

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using bw model

Run on: July 7, 2005, 14:30:40 ; Search time 76 Seconds
(without alignments)

37.980 Million cell updates/sec

Title: US-10-724-532-1

Perfect score: 150

Sequence: 1 QARONLQNLFINFCLILCLILICILIVML 30

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: pir79: *
2: pir1: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	150	100.0	52	1 A29002	phospholamban - do
2	150	100.0	52	1 A49057	phospholamban - mo
3	150	100.0	52	1 B40424	phospholamban - ra
4	150	100.0	52	1 S05440	phospholamban - pi
5	150	100.0	52	1 S37638	phospholamban - ra
6	144	96.0	52	1 A40424	phospholamban - hu
7	137	91.3	52	1 A39535	phospholamban - ch
8	58.5	39.0	305	2 T34239	hypothetical prote
9	57	38.0	69	2 A81445	probable integral
10	55	36.7	169	2 T08827	hypothetical prote
11	53	35.3	431	2 B97277	probable O-antigen
12	53	35.3	573	2 I40496	methylation enzyme
13	53	35.3	1880	2 T18531	cractin - medicina
14	52.5	35.0	77	1 MN1M3	nonstructural prot
15	52.5	35.0	77	1 S25709	hypothetical prote
16	52	34.7	80	2 T28256	ORF MSV095 hypote
17	52	34.7	354	2 T32319	hypothetical prote
18	52	34.7	382	2 T41256	hypothetical ryan
19	52	34.7	396	2 AH1421	efflux protein hom
20	52	34.7	1014	2 H71602	protein with dnuu
21	52	34.7	1182	2 T13952	membrane protein p
22	51	34.0	458	2 F86433	protein T17H7.5 (l
23	51	34.0	584	2 JC7809	sulfakinin recepto
24	51	34.0	858	2 JC7683	taase receptor T1R
25	50.5	33.7	177	2 B70156	probable chromate
26	50.5	33.7	388	2 C81568	hypothetical prote
27	50.5	33.7	388	2 H86520	hypothetical prote
28	50	33.3	211	2 B56691	mpal 5'-region hyp
29	50	33.3	226	1 JQ1570	major surface anti

30	50	33.3	226	2 JQ2058	surface antigen -
31	50	33.3	226	2 JQ2061	surface antigen -
32	50	33.3	226	2 JQ2060	surface antigen -
33	50	33.3	226	2 JQ2057	surface antigen -
34	50	33.3	226	2 JQ2062	surface antigen -
35	50	33.3	226	2 JQ2059	surface antigen -
36	50	33.3	348	2 JC7907	common cytokine re
37	50	33.3	359	2 B59105	hypothetical prote
38	50	33.3	378	2 T34372	hypothetical prote
39	50	33.3	388	2 E72103	hypothetical prote
40	50	33.3	389	1 SAVLJ1	large surface anti
41	50	33.3	389	1 SAVLJ2	large surface anti
42	50	33.3	389	1 SAVLJ3	large surface anti
43	50	33.3	484	2 C88264	protein kin-15 (lm
44	50	33.3	488	2 I44330	protein-tyrosine k
45	50	33.3	511	2 F86460	probable cytochrom

ALIGNMENTS

RESULT 1
A29002
phospholamban - dog
C:Species: Canis lupus familiaris (dog)
C:Date: 23-Aug-1987 #sequence revision 27-Jun-1994 #text_change 09-Jul-2004
C:Accession: A29002; A26805; A25307; A24818; I46227
R:Fujii, J.; Ueno, A.; Kitano, K.; Tanaka, S.; Kadoma, M.; Tada, M.
J. Clin. Invest. 79, 301-304, 1987
A:Title: Complete complementary DNA-derived amino acid sequence of canine cardiac phospholamban
A:Reference number: A29002; MUID:87083954; PMID:3793929
A:Accession: A29002
A:Molecule type: mRNA
A:Residues: 1-52 <RUI>
A:Cross-references: UNIPROT:P61012; GB:M16012; NID:G164043; PIND:AAA30884.1; PID:G164044
R:Uyeda, A.; Kitano, K.; Fujii, J.; Kadoma, M.; Tada, M.; Tanaka, S.
Nucleic Acids Res. 15, 6738, 1987
A:Title: The cDNA sequence of the major phospholamban mRNA in canine cardiac ventricular
A:Reference number: A26805; MUID:87316936; PMID:3628007
A:Accession: A26805
A:Molecule type: mRNA
A:Residues: 1-52 <MYB>
A:Cross-references: GB:Y00399; NID:G911; PIND:CAA68461.1; PID:G912
R:Simmerman, H.K.B.; Collins, J.H.; Theibert, J.L.; Wegener, A.D.; Jones, L.R.
J. Biol. Chem. 261, 13333-13341, 1986
A:Title: Sequence analysis of phospholamban. Identification of phosphorylation sites and
A:Reference number: A25307; MUID:87008549; PMID:3759968
A:Contents: partial sequence and phosphorylation sites
A:Accession: A25307
A:Molecule type: protein
A:Residues: 10-45 <SIM>
R:Fujii, J.; Kadoma, M.; Tada, M.; Toda, H.; Sakiyama, F.
Biochem. Biophys. Res. Commun. 138, 1044-1050, 1986
A:Title: Characterization of structural unit of phospholamban by amino acid sequencing
A:Reference number: A24818; MUID:86323152; PMID:3753485
A:Contents: partial sequence and acetylation site
A:Accession: A24818
A:Molecule type: protein
A:Residues: 1-35, 'X', 'Y', '37-40', 'X', '42-45' <FUG>
R:Uyeda, A.; Kitano, K.; Fujii, J.; Kadoma, M.; Tada, M.; Tanaka, S.
Nucleic Acids Symp. Ser. 17, 121-124, 1986
A:Title: Characterization of recombinant cDNA clones for canine cardiac phospholamban.
A:Reference number: I46227; MUID:87174860; PMID:3562256
A:Accession: I46227
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-52 <UY2>
A:Cross-references: NID:G164045; PIND:AA41618.1; PID:G164046
C:Comment: Phospholamban is expressed in cardiac muscle, slow twitch skeletal muscle, ar
e, after phosphorylation, the Ca++ pump is activated and the rate of muscle relaxation i
C:Superfamily: cardiac phospholamban
C:Keywords: acetylated amino end; ATPase inhibitor; muscle; pentamer; phosphoprotein; ci

F,31-52/Domain: transmembrane #status predicted <TM>
 F,1/Modified site: acetylated amino end (Met) #status experimental
 F,16/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status experiment
 F,17/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) #status experiment

Query Match 100.0%; Score 150; DB 1; Length 52;
 Best Local Similarity 100.0%; Pred. No. 2,9e-11;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QARQNLQNLFTNFCILICLLICITIVML 30
 Db 23 QARQNLQNLFTNFCILICLLICITIVML 52

RESULT 2

A49057

phospholamban - mouse

C,Species: Mus musculus (house mouse)

C,Date: 19-Dec-1993 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004

C,Accession: A49057

R,Genim, J.R.; Luo, W.; Ponniah, S.; Grupp, I.; Kim, H.W.; Ferguson, D.G.; Kadambi, V.;

Circ. Res. 71, 1021-1030, 1992

A,Title: Mouse phospholamban gene expression during development in vivo and in vitro.

A,Reference number: A49057; PMID:93008602; PMID:1394867

A,Accession: A49057

A,Molecule type: mRNA

A,Cross-references: UNIPROT:P61014; GB:S46792; NID:G257745; PIDN:AA23706.1; PID:G257746

A,Experimental source: cardiac muscle

A,Note: Sequence extracted from NCBI backbone (NCBI:116999, NCBI:117001)

C,Comment: Phospholamban is expressed in cardiac muscle, slow twitch skeletal muscle, an

e; after phosphorylation, the Ca++ pump is activated and the rate of muscle relaxation i

C,Superfamily: cardiac phospholamban

C,Keywords: acetylated amino end; ATPase inhibitor; muscle; pentamer; phosphoprotein; tr

F,31-52/Domain: transmembrane #status predicted <TM>

F,1/Modified site: acetylated amino end (Met) #status predicted

F,16/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predict

F,17/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) #status p

Query Match 100.0%; Score 150; DB 1; Length 52;
 Best Local Similarity 100.0%; Pred. No. 2,9e-11;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QARQNLQNLFTNFCILICLLICITIVML 30
 Db 23 QARQNLQNLFTNFCILICLLICITIVML 52

RESULT 3

B40424

phospholamban - rabbit

C,Species: Oryctolagus cuniculus (domestic rabbit)

C,Date: 28-Feb-1992 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004

C,Accession: B40424; S00249

R,Fujii, J.; Zairain-Herzberg, A.; Willard, H.F.; Tada, M.; MacLennan, D.H.

J. Biol. Chem. 266, 11669-11675, 1991

A,Title: Structure of the rabbit phospholamban gene, cloning of the human cDNA, and asse

A,Reference number: A40424; PMID:91268032; PMID:1828805

A,Accession: B40424

A,Molecule type: DNA

A,Residues: 1-52 <FU>

A,Cross-references: UNIPROT:P61015; GB:M63601; NID:G165636; PIDN:AAA1445.1; PID:G165639

R,Fujii, J.; Lytton, J.; Tada, M.; MacLennan, D.H.

FEBS Lett. 227, 51-55, 1988

A,Title: Rabbit cardiac and slow-twitch muscle express the same phospholamban gene.

A,Reference number: S00249; PMID:8811222; PMID:2962883

A,Accession: S00249

A,Status: not compared with conceptual translation

C,Comment: Phospholamban is the major phosphorylated protein in cardiac muscle sarcoplas
 e; after phosphorylation, the Ca++ pump is activated and the rate of muscle relaxation i
 C,Genetics:
 A,Note: only one gene was detected

C,Superfamily: cardiac phospholamban

C,Keywords: acetylated amino end; ATPase inhibitor; muscle; pentamer; phosphoprotein; tr

F,31-52/Domain: transmembrane #status predicted <TM>

F,1/Modified site: acetylated amino end (Met) #status predicted

F,16/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predict

F,17/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) #status p

Query Match 100.0%; Score 150; DB 1; Length 52;
 Best Local Similarity 100.0%; Pred. No. 2,9e-11;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QARQNLQNLFTNFCILICLLICITIVML 30
 Db 23 QARQNLQNLFTNFCILICLLICITIVML 52

RESULT 4

S05540

phospholamban - pig

C,Species: Sus scrofa domestica (domestic pig)

C,Date: 21-Nov-1993 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004

C,Accession: S05540

R,Verboom, H.; Muytack, F.; Eggermont, J.A.; de Jaegere, S.; Misslaen, L.; Raeymaekers

Biochem. J. 262, 353-356, 1989

A,Title: cDNA cloning and sequencing of phospholamban from pig stomach smooth muscle.

A,Reference number: S05540; PMID:90056437; PMID:2530978

A,Accession: S05540

A,Molecule type: mRNA

A,Cross-references: UNIPROT:P61013; EMBL:X15075; NID:G2055; PIDN:CAA3171.1; PID:G2056

C,Comment: Phospholamban is expressed in cardiac muscle, slow twitch skeletal muscle, an

e; after phosphorylation, the Ca++ pump is activated and the rate of muscle relaxation i

C,Superfamily: cardiac phospholamban

C,Keywords: acetylated amino end; ATPase inhibitor; muscle; pentamer; phosphoprotein; tr

F,31-52/Domain: transmembrane #status predicted <TM>

F,1/Modified site: acetylated amino end (Met) #status predicted

F,16/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predict

F,17/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) #status p

Query Match 100.0%; Score 150; DB 1; Length 52;
 Best Local Similarity 100.0%; Pred. No. 2,9e-11;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QARQNLQNLFTNFCILICLLICITIVML 30
 Db 23 QARQNLQNLFTNFCILICLLICITIVML 52

RESULT 5

S37638

phospholamban - rat

C,Species: Rattus norvegicus (Norway rat)

C,Date: 05-Mar-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004

C,Accession: S37638; I52270; I64795; I51940

R,Shanahan, C.M.; Weisberg, P.U.; Metcalfe, J.C.

Circ. Res. 73, 193-204, 1993

A,Title: Isolation of gene markers of differentiated and proliferating vascular smooth m

A,Reference number: S37637; PMID:93284726; PMID:8508530

A,Accession: S37638

A,Molecule type: mRNA

A,Residues: 1-52 <SHA>

A,Cross-references: UNIPROT:P61016; EMBL:X71068; NID:G313809; PIDN:CAA50394.1; PID:G3138

```

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-52 <JOH>
A:Cross-references: GB:103382; NID:g206134; PION:AAA41849.1; PID:g206136
R:Wang, K.S.; Nadal-Ginard, B.
Adv. Exp. Med. Biol. 304, 387-395, 1991
A:Title: Cloning phospholamban cDNA from rat aortic smooth muscle.
A:Reference number: 151840; MUID:92206263; PMID:1725098
A:Accession: 164795
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-52 <HWAL>
A:Cross-references: GB:S95853; NID:g247932; PIDN:AAB21903.1; PID:g247933
A:Accession: 151840
A:Molecule type: translated from GB/EMBL/DBJ
A:Residues: 1-52 <HWAL>
A:Cross-references: GB:S95849; NID:g247934
C:Comment: Phospholamban is expressed in cardiac muscle, slow twitch skeletal muscle, an
C:Comment: Phospholamban is the major phosphorylated protein in cardiac muscle sarcoplas
Pase; after phosphorylation, the calcium pump is activated and the rate of muscle relax
C:Superfamily: cardiac phospholamban
C:Keywords: acetylated amino end; ATPase inhibitor; cardiac muscle; heart; pentamer; pho
F:31-52/Domain: transmembrane #status predicted <TMM>
F:16/Binding site: acetylated amino end (Met) #status predicted
F:17/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) #status p
Query Match 100.0%; Score 150; DB 1; Length 52;
Best Local Similarity 100.0%; Pred. No. 2, 9e-11;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 QARQNLQNLFFNFCILICLLICILIVML 30
23 QARQNLQNLFFNFCILICLLICILIVML 52

```

```

RESULT 7
A39535
phospholamban - chicken
C:Species: Gallus gallus (chicken)
C:Date: 06-Mar-1992 #sequence revision 27-Jun-1994 #text_change 09-Jul-2004
C:Accession: A39535; B39535; A44531
R:Toyofuku, T.; Zak, R.
J. Biol. Chem. 266, 5375-5383, 1991
A:Title: Characterization of cDNA and genomic sequences encoding a chicken phospholamban
A:Reference number: A39535; MUID:91170195; PMID:1825996
A:Accession: A39535
A:Molecule type: mRNA
A:Residues: 1-17, 19-52 <TOY>
A:Cross-references: UNIPROT:P26677; GB:M59039; NID:g212575; PION:AAA62738.1; PID:g212576
A:Note: the authors translated the codon CTT for residue 18 as Ile
A:Accession: B39535
A:Molecule type: DNA
A:Residues: 1-52 <TO2>
A:Cross-references: GB:M59038
A:Note: the sequence of residues 33-52 and the corresponding nucleotide sequence are not
R:Toyofuku, T.; Zak, R.
submitted to Genbank, April 1991
A:Reference number: A44531
A:Accession: A44531
A:Molecule type: DNA
A:Residues: 1-52 <TO3>
A:Cross-references: GB:M59038
C:Comment: Phospholamban is expressed in cardiac muscle, slow twitch skeletal muscle, an
C:Comment: Phospholamban is the major phosphorylated protein in cardiac muscle sarcoplas
e; after phosphorylation, the Ca++ pump is activated and the rate of muscle relaxation i
C:Genetics:
A:Note: only one gene was detected
A:Note: the single intron is upstream of the coding region
C:Superfamily: cardiac phospholamban
C:Keywords: acetylated amino end; ATPase inhibitor; muscle; pentamer; phosphoprotein; tr
F:31-52/Domain: transmembrane #status predicted <TMM>
F:16/Binding site: acetylated amino end (Met) #status predicted
F:17/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) #status p
Query Match 91.3%; Score 137; DB 1; Length 52;
Best Local Similarity 90.0%; Pred. No. 9, 9e-10;
Matches 27; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
1 QARQNLQNLFFNFCILICLLICILIVML 30
23 QARQNLQNLFFNFCILICLLICILIVML 52

```

```

RESULT 8
T34299
hypothetical protein F54E7.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T34299
R:Bentley, D.
submitted to the EMBL Data Library, June 1994
A:Description: The sequence of C. elegans cosmid F54E7.
A:Reference number: 221502
A:Accession: T34299
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-305 <BEN>
A:Cross-references: UNIPROT:Q20783; EMBL:U00067; PION:AACT7517.1; GSPDB:GN00021; CESP:F5
C:Genetics:
A:Experimental source: strain Bristol N2; clone F54E7
A:Gene: CESP:F54E7.5
A:Map position: 3
A:Introns: 78/3; 173/3
Query Match 96.0%; Score 144; DB 1; Length 52;
Best Local Similarity 96.7%; Pred. No. 1, 5e-10;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
1 QARQNLQNLFFNFCILICLLICILIVML 30
23 QARQNLQNLFFNFCILICLLICILIVML 52

```

Best Local Similarity 54.2%; Pred. No. 6;
Matches 13; Conservative 3; Mismatches 7; Indels 1; Gaps 1;
OY 7 ONLFINPCLILICILICIIWML 30
Db 186 QHLLI-ACLILICLITFCIIIVFI 208

RESULT 9

AB1445

probable integral membrane protein Cj0266c [imported] - Campylobacter jejuni (strain NCTC13627)

C:Species: Campylobacter jejuni
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004

A:Accession: AB1445
R:Packhill, J.; Wren, B.W.; Mungall, K.; Kestley, J.M.; Churcher, C.; Baaham, D.; Chillingworth, C.W.; O'Neill, M.; Rajandream, M.A.; Rutherford, K.M.; VanVleet, A.; Whitehead, S.; Barrell

Nature 403, 665-668, 2000
A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals h

A:Reference number: AB1250; MUID:20150912; PMID:10688204
A:Accession: AB1250

A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-169 <PAR>
A:Cross-references: UNIPROT:O9PTM9; GB:AL139074; GB:AL111168; NID:g6967505; PIDN:CAB7273

A:Experimental source: serotype O2, strain NCTC 1168
C:Genetics:

A:Gene: Cj0266c
C:Superfamily: Campylobacter jejuni probable integral membrane protein Cj0266c

Query Match 38.0%; Score 57; DB 2; Length 169;
Best Local Similarity 52.6%; Pred. No. 5.8;
Matches 10; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

OY 11 INFCLILICILICIIWML 29
Db 9 IAFILICFALICILIFL 27

RESULT 10
T08827
hypothetical protein cotel - human
C:Species: Homo sapiens (man)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004

C:Accession: T08827
R:Winfeld, S.V.; Tayebi, N.; Martin, B.M.; Gimn, E.I.; Sidransky, E.

Genome Res. 7, 1020-1026, 1997
A:Title: Identification of three additional genes contiguous to the glucocerebrosidase 1

A:Reference number: Z16482; MUID:97474796; PMID:9331372
A:Accession: T08827

A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA

A:Residues: 1-669 <WIN>
A:Cross-references: UNIPROT:P81408; EMBL:AF023266; NID:g5564910; PIDN:AMC51822.1; PID:g2

C:Genetics:
A:Gene: cotel

A:Map position: 1
A:introns: 75/3; 94/3; 131/3; 171/3; 207/3; 266/2; 299/3; 323/1; 505/1; 528/1; 612/3

Query Match 36.7%; Score 55; DB 2; Length 669;
Best Local Similarity 38.5%; Pred. No. 27;
Matches 10; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

OY 1 QARQNLQNLFINPCLILICILICII 26
Db 165 EARGALKLPSVCGLTICAITCRL 190

RESULT 11
B97277
probable O-antigen/teichoic acid transporter CAC3065 [imported] - Clostridium acetobutylicum

C:Species: Clostridium acetobutylicum
C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C:Accession: B97277

R.Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.C.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.

J. Bacteriol. 183, 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo

A:Reference number: A96900; MUID:21359325; PMID:21359325
A:Accession: B97277

A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-431 <KUN>
A:Cross-references: UNIPROT:Q97EP3; GB:AE001437; PIDN:AAK81005.1; PID:g15026127; GSPDB:G

A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:

A:Gene: CAC3065
C:Superfamily: O-antigen transporter protein

Query Match 35.3%; Score 53; DB 2; Length 431;
Best Local Similarity 32.1%; Pred. No. 34;
Matches 9; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

OY 3 QNLQNLFINPCLILICILICIIWML 30
Db 83 KKIEIEFNSVWLKALITFCIIIVLV 110

RESULT 12
140496
methyl-accepting chemotaxis protein Cj0266c

N:Alternate names: 62k MCP-like protein TlPC; methyl-accepting chemotaxis protein TlPC

C:Species: Bacillus subtilis
C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004

A:Accession: 140496; B69724; E45067
R:Hanlon, D.W.; Rosario, M.W.; Ordal, G.W.; Venema, G.; Van Sinderen, D.

Microbiology 140, 1847-1854, 1994
A:Title: Identification of TlPC, a novel 62 kDa MCP-like protein from Bacillus subtilis.

A:Reference number: 140495; MUID:95005439; PMID:7921238
A:Accession: 140496

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA

A:Residues: 1-573 <RES>
A:Cross-references: UNIPROT:P39209; EMBL:Z34005; NID:g496483; PIDN:CAA83970.1; PID:g4964

R:Kunst, F.; Ogasawara, N.; Moser, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter, C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capiano, V.; Carter, N.M.; Cho

A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.

Nature 350, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fuma, S.; Galizzi, A.; Galler

ich, J.; Harwood, C.R.; Henauc, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.

Koster, P.; Koningslein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.

Authors: Lamber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel

Y, M.; Ogawa, K.; Ogilvara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetle

Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon, A.

Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serot

akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpetra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.

Winers, P.; Wipet, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K

A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.

A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.

A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: B69724

A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA

A:Residues: 1-215, 'T', 217-331, 'P', 333-573 <KUN>
A:Cross-references: GB:Z59105; GB:AL009126; NID:g2632457; PIDN:CAB12138.1; PID:g2632630

A:Experimental source: strain 168
C:Genetics:

A:Gene: tlPC
C:Superfamily: methyl-accepting chemotaxis protein

Query Match 35.3%; Score 53; DB 2; Length 573;
Best Local Similarity 29.2%; Pred. No. 42;
Matches 7; Conservative 12; Mismatches 5; Indels 0; Gaps 0;

OY 7 ONLFINPCLILICILICIIWML 30
Db 183 QSLFQFAIVLIVIMVSVILVLV 206

RESULT 13

T18531

tractin - medicinal leech

C/Species: Hirudo medicinalis (medicinal leech)

C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C/Accession: T18531

R/Huang, Y.; Jellies, J.; Johansen, K.M.; Johansen, J.

J. Cell Biol. 138, 143-157, 1997

A/Title: Differential glycosylation of Tractin and LeechCAM, two novel Ig-superfamily me

A/Reference number: Z18951; MUID:97362067; PMID:9214388

A/Accession: T18531

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-1880 <HUA>

A/Cross-references: UNIPROT:O18465; EMBL:U92813; NID:G2275259; PID:G2275260; PIDN:AAC476

Query Match

Best Local Similarity 35.3%; Score 53; DB 2; Length 1880;

Matches 8; Conservative 9; Mismatches 2; Indels 0; Gaps 0;

QY 12 NPLILICLLICIIIVML 30

DB 1751 NWLILICLLILLLIL 1769

RESULT 14

NM1H3

nonstructural protein 5B - human coronavirus (strain 229E)

C/Species: human coronavirus

C/Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 09-Jul-2004

C/Accession: C34038

R/Rabe, T.; Siddell, S.

Nucleic Acids Res. 17, 6387, 1989

A/Title: Nucleotide sequence of the human coronavirus HCV 229E mRNA 4 and mRNA 5 unique

A/Reference number: A34038; MUID:89366667; PMID:2701946

A/Accession: C34038

A/Molecule type: genomic RNA

A/Residues: 1-77 <RAA>

A/Cross-references: UNIPROT:P19741; EMBL:X15654; NID:G58921; PIDN:CAA33684.1; PID:G58925

C/Superfamily: coronavirus nonstructural protein 5B

C/Keywords: nonstructural protein

Query Match 35.0%; Score 52.5; DB 1; Length 77;

Best Local Similarity 40.0%; Pred. No. 11;

Matches 10; Conservative 8; Mismatches 4; Indels 3; Gaps 1;

QY 9 LEIN---FCLILICLLICIIIVML 30

DB 11 LVNVVLMVCVILVILVLCITIKL 35

RESULT 15

S25709

hypohectical protein 5 - human coronavirus

C/Species: human coronavirus 229E

C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 18-Jul-2001

C/Accession: S25709

R/Jouvenne, P.; Mount, S.; Stewart, J.N.; Richardson, C.D.; Talbot, P.J.

Virus Res. 22, 125-141, 1992

A/Title: Sequence analysis of human coronavirus 229E mRNAs 4 and 5: evidence for polymor

A/Reference number: S25708; MUID:92230395; PMID:1373555

A/Accession: S25709

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-77 <YOU>

A/Cross-references: EMBL:X64942; NID:G59462; PIDN:CAA46114.1; PID:G59464

C/Superfamily: coronavirus nonstructural protein 5B

Query Match 35.0%; Score 52.5; DB 2; Length 77;

Best Local Similarity 40.0%; Pred. No. 11;

Matches 10; Conservative 8; Mismatches 4; Indels 3; Gaps 1;

QY 9 LEIN---FCLILICLLICIIIVML 30
DB 11 LVNVVLMVCVILVILVLCITIKL 35

Search completed: July 7, 2005, 15:42:30
Job time : 77 secs

This Page Blank (uspto)

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rnp**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 7, 2005, 12:19:31 ; Search time 394 Seconds
(without alignments)

38.991 Million cell updates/sec

Title: US-10-724-532-1

Perfect score: 150
Sequence: 1 QARONLQNLFINFCILICLLICILIVML 30

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: uniprot_03:*
2: uniprot_sprot:*
3: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	150	100.0	52	1 PPLA_CANFA	P61012 canis fam1
2	150	100.0	52	1 PPLA_MOUSE	P61014 mus musculu
3	150	100.0	52	1 PPLA_PIG	P61013 sus scrofa
4	150	100.0	52	1 PPLA_RABIT	P61015 oryctolagus
5	150	100.0	52	1 PPLA_RAT	P61016 rattus norv
6	144	96.0	52	1 PPLA_HUMAN	P26677 homo sapien
7	137	91.3	52	1 PPLA_CHICK	P26677 gallus gall
8	59.5	39.7	792	2 Q07816	Q07816 caenorhabd
9	58.5	39.0	305	2 Q07813	Q07813 mus musculu
10	58	38.7	31	1 SARL_MOUSE	Q9cqd6 mus musculu
11	58	38.7	31	2 Q6SLB7	Q6SLB7 rattus norv
12	57.5	38.3	130	2 Q70V94	Q70V94 cotesia kaz
13	57	38.0	169	2 Q9PIM9	Q9PIM9 campylobact
14	56	37.3	35	2 Q6VZB7	Q6VZB7 bidesodes
15	56	37.3	110	2 Q8BS41	Q8BS41 mus musculu
16	56	37.3	268	2 Q801W9	Q801W9 equash leat
17	56	37.3	357	2 Q8EWJ5	Q8EWJ5 mycoplasma
18	56	37.3	422	1 K3L1_RAT	P83556 rattus norv
19	56	37.3	4638	2 Q8IK66	Q8IK66 plasmodium
20	55.5	37.0	130	2 Q70V90	Q70V90 cotesia oro
21	55.5	37.0	218	2 Q6RF12	Q6RF12 cotesia oro
22	55.5	37.0	400	2 Q8DKW1	Q8DKW1 streptococ
23	55.5	37.0	400	2 Q8EB10	Q8EB10 streptococ
24	55	36.7	31	1 SARL_HUMAN	Q00631 homo sapien
25	55	36.7	122	2 Q8R0C6	Q8R0C6 mus musculu
26	55	36.7	364	2 Q896T0	Q896T0 clostridium
27	55	36.7	369	2 Q813E8	Q813E8 bacillus an
28	55	36.7	394	2 Q6H078	Q6H078 bacillus an
29	55	36.7	668	2 Q9BR66	Q9BR66 homo sapien
30	55	36.7	669	1 COTE_HUMAN	P81408 homo sapien
31	54	36.0	326	2 Q6GN07	Q6GN07 xenopus lae

32	54	36.0	433	1 PIGU_MOUSE	Q8K358 mus musculu
33	54	36.0	434	1 PIGU_HUMAN	Q9H490 homo sapien
34	54	36.0	434	1 PIGU_RAT	Q8CHJ1 rattus norv
35	54	36.0	482	2 Q9MG49	Q9MG49 chrysodidym
36	54	36.0	513	2 Q675R3	Q675R3 oikopleura
37	54	36.0	720	2 Q40902	Q40902 pecunia int
38	53.5	35.7	130	2 Q70V97	Q70V97 cotesia fla
39	53.5	35.7	217	2 Q6EF08	Q6EF08 cotesia mei
40	53.5	35.7	217	2 Q6EF10	Q6EF10 cotesia mei
41	53	35.3	113	2 Q8CBJ2	Q8CBJ2 mus musculu
42	53	35.3	245	2 Q7SME1	Q7SME1 ovine enzoo
43	53	35.3	245	2 Q7SME2	Q7SME2 ovine enzoo
44	53	35.3	263	2 Q925D4	Q925D4 rattus norv
45	53	35.3	263	2 Q9WU52	Q9WU52 mus musculu

ALIGNMENTS

RESULT 1
PPLA_CANFA STANDARD; PRT; 52 AA.
ID PPLA_CANFA
AC P61012; P07473; 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Cardiac phospholamban (PLB).
GN Name=PLN;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OC NCBI_Taxid=9615;
RN [1]
RP MEDLINE=87083954; PubMed=3793929;
RA Fujii J., Ueno A., Kitano K., Tanaka S., Kadoma M., Tada M.,
RT "Complete complementary DNA-derived amino acid sequence of canine
cardiac phospholamban.";
RL J. Clin. Invest. 79:301-304(1987).
RN [2]
RP TISSUE=Heart ventricle;
RX MEDLINE=87316936; PubMed=3628007;
RA Uyeda A., Kitano K., Fujii J., Kadoma M., Tada M., Tanaka S.;
RT "The cDNA sequence of the major phospholamban mRNA in canine cardiac
ventricular muscle.";
RL Nucleic Acids Res. 15:6738-6738(1987).
RN [3]
RP SEQUENCE OF 1-45, AND ACETYLATION.
RX MEDLINE=86323152; PubMed=3753485;
RA Fujii J., Kadoma M., Tada M., Toda H., Sakiyama F.;
RT "Characterization of structural unit of phospholamban by amino acid
sequencing and electrophoretic analysis.";
RL Biochem. Biophys. Res. Commun. 138:1044-1050(1986).
RN [4]
RP SEQUENCE OF 10-45, AND PHOSPHORYLATION SITES SER-16 AND THR-17.
RX MEDLINE=87008549; PubMed=3759568;
RA Simerman H.K.B., Collins J.H., Theibert J.L., Wegener A.D.,
RA Jones L.R.;
RT "Sequence analysis of phospholamban. Identification of phosphorylation
sites and two major structural domains.";
RL J. Biol. Chem. 261:13333-13341(1986).
RN [5]
RP PHOSPHORYLATION SITES SER-16 AND THR-17.
RX MEDLINE=89291905; PubMed=2544595;
RA Wegener A.D., Simerman H.K.B., Lindemann J.P., Jones L.R.;
RT "Phospholamban phosphorylation in intact ventricles. Phosphorylation
of serine 16 and threonine 17 in response to beta-adrenergic
stimulation.";
RL J. Biol. Chem. 264:11468-11474(1989).
CC -1- FUNCTION: Phospholamban has been postulated to regulate the
activity of the calcium pump of cardiac sarcolemmal reticulum.
CC -1- SUBUNIT: Homopentamer.

```

CC -1- SUBCELLULAR LOCATION: Membrane.
CC -1- TISSUE SPECIFICITY: Heart.
CC -1- PM: Phosphorylated in response to beta-adrenergic stimulation.
CC -1- SIMILARITY: Belongs to the phospholamban family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M16012; AAA0884.1; -
DR EMBL; Y00399; CA68461.1; -
DR EMBL; M35393; AAC41618.1; -
DR PIR; A29002; A29002.
DR InterPro; IPR005984; P_lamban.
DR PIRSF; PIRSF001665; PLB; 1.
DR TIGRFAMs; TIGR01294; P_lamban; 1.
KW Acetylation; Direct protein sequencing; Phosphorylation;
KW Transmembrane.
FT DOMAIN 1 31 Cytoplasmic (Potential).
FT TRANSMEM 32 52 Potential.
FT MOD_RES 1 1 N-acetylmethionine.
FT MOD_RES 16 16 Phosphoserine (by PKA).
FT MOD_RES 17 17 Phosphothreonine (by CAMK1).
SQ SEQUENCE 52 AA; 6080 MW; 076351D9ADCA24D3 CRC64;

Query Match 100.0%; Score 150; DB 1; Length 52;
Best Local Similarity 100.0%; Pred. No. 1,2e-10;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 QARQNLQNLFFNFCILICLLICILICIVML 30
Db 23 QARQNLQNLFFNFCILICLLICILICIVML 52

RESULT 2
PPLA_MOUSE STANDARD; PRT; 52 AA.
AC P61014; P20006;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Cardiac phospholamban (PLB).
GN Name=Pln;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=93008802; PubMed=1394867;
RA Gailin J.R., Luo W., Ponniah S., Grupp I., Kim H.W., Ferguson D.G.,
RA Kadambi V., Neumann J.C., Doetschman T., Kranias E.G.;
RT "Mouse phospholamban gene expression during development in vivo and in
RT vitro";
RL Cite. Res. 71:1021-1030(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Aorta, Heart, and Kidney;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Mikaido I., Oatso N., Saito R., Suzuki H., Yamataka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gotohori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schirni L.M., Kanapin A., Matsuda A., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Busnic V., Chochia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frizer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,

```

```

RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Koenig A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numa K., Okido T., Pavan M.J., Petrea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontus J.U., Qi D., Ramchandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sempke C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Veraldo R., Wagner L., Walstedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Komio H., Nakamura M., Sakazune N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.,
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hestef F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshimiyuki S., Carninci P., Frange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Huliyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Keeton M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Boulford G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- FUNCTION: Phospholamban has been postulated to regulate the
CC activity of the calcium pump of cardiac sarcoplasmic reticulum.
CC -1- SUBUNIT: Homopentamer (By similarity).
CC -1- SUBCELLULAR LOCATION: Membrane (By similarity).
CC -1- PM: Phosphorylated in response to beta-adrenergic stimulation (By
CC similarity).
CC -1- SIMILARITY: Belongs to the phospholamban family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; S46792; AAB23706.1; -
DR EMBL; AK002622; BAB22237.1; -
DR EMBL; AK040718; BAC00680.1; -
DR EMBL; AK052199; BAC34880.1; -
DR EMBL; BC061097; AAB61097.1; -
DR PIR; A49057; A49057.
DR HSSP; P07473; IFUK.
DR MGD; MGI:97622; Pln.
DR InterPro; IPR005984; P_lamban.
DR PIRSF; PIRSF001665; PLB; 1.
DR TIGRFAMs; TIGR01294; P_lamban; 1.
KW Acetylation; Phosphorylation; Transmembrane.
KW DOMAIN 1 31 Cytoplasmic (Potential).

```

```

FT TRANSMEM 32 52 Potential.
FT MOD_RES 1 1 N-acetylmethionine (By similarity).
FT MOD_RES 16 16 Phosphoserine (by PKA) (By similarity).
FT MOD_RES 17 17 Phosphothreonine (by CamK) (By
SQ SEQUENCE 52 AA; 6094 MW; 0763601F76A854D3 CRC64;

Query Match 100.0%; Score 150; DB 1; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QARONLQNFNFCLILCLILCLILCLILCLIL 30
Db 23 QARONLQNFNFCLILCLILCLILCLILCLIL 52

RESULT 3
PPLA_PIG STANDARD; PRT; 52 AA.
AC P61013; P07473;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Cardiac phospholamban (PLB).
GN Name=PLN;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Smooth muscle;
RX MEDLINE=90056437; PubMed=2530978;
RA Verboom H., Muyck F., Eggermont J.A., de Jaegere S., Misaen L.,
RA Raeymaekers L., Castels R.;
RT "cDNA cloning and sequencing of phospholamban from pig stomach smooth
RT muscle.";
RN Biochem. J. 262:353-356(1989).
RL [2]
RP STRUCTURE BY NMR.
RA Lamberth S., Griesinger C., Schmid H., Carafoli E., Muenchbach M.,
RA Vorreiter T., Krebs J.;
RT "NMR solution structure of phospholamban membrane protein.";
RT Submitted (Aug-2000) to the PDB data bank.
CC -1- FUNCTION: Phospholamban has been postulated to regulate the
CC activity of the calcium pump of cardiac sarcoplasmic reticulum.
CC -1- SUBUNIT: Homopentamer (By similarity).
CC -1- SUBCELLULAR LOCATION: Membrane (By similarity).
CC -1- PTM: Phosphorylated in response to beta-adrenergic stimulation (By
CC similarity).
CC -1- SIMILARITY: Belongs to the phospholamban family.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
CC EMBL, X15075; CAA33171.1; -.
CC DR PIR; S05540; S05540.
CC DR PDB; 1FJK; NMR; -.
CC DR InterPro; IPR005984; P_lamban.
CC DR PIRSF; PIRSF001665; PLB; 1.
CC DR TIGRFAWS; TIGR01294; P_lamban; 1.
CC DR 3D-structure; Acetylation; Phosphorylation; Transmembrane.
CC FT DOMAIN 1 31 Cytoplasmic (Potential).
CC FT TRANSMEM 32 52 Potential.
CC FT MOD_RES 1 1 N-acetylmethionine (By similarity).
CC FT MOD_RES 16 16 Phosphoserine (by PKA) (By similarity).
CC FT MOD_RES 17 17 Phosphothreonine (by CamK) (By
similarity).

```

```

FT HELIX 4 16
FT MOD_RES 21 49
FT TURN 50 52
SQ SEQUENCE 52 AA; 6080 MW; 076361D9ADC424D3 CRC64;

Query Match 100.0%; Score 150; DB 1; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QARONLQNFNFCLILCLILCLILCLILCLIL 30
Db 23 QARONLQNFNFCLILCLILCLILCLILCLIL 52

RESULT 4
PPLA_RABIT STANDARD; PRT; 52 AA.
AC P61015; P20006;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Cardiac phospholamban (PLB).
GN Name=PLN;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=91288032; PubMed=1828805;
RA Fujii J., Zarain-Herzberg A., Willard H.F., Tada M., MacLennan D.H.;
RA Fujii J., Lytton J., Tada M., MacLennan D.H.;
RT "Structure of the rabbit phospholamban gene, cloning of the human
RT cDNA, and assignment of the gene to human chromosome 6.";
RN J. Biol. Chem. 266:11669-11675(1991).
RL [2]
RP SEQUENCE FROM N.A.
RC MEDLINE=88112222; PubMed=2962883; DOI=10.1016/0014-5793(88)81412-1;
RA Fujii J., Lytton J., Tada M., MacLennan D.H.;
RT "Rabbit cardiac and slow-twitch muscle express the same phospholamban
RT gene.";
RN FEBS Lett. 227:51-55(1988).
RL [2]
CC -1- FUNCTION: Phospholamban has been postulated to regulate the
CC activity of the calcium pump of cardiac sarcoplasmic reticulum.
CC -1- SUBUNIT: Homopentamer.
CC -1- SUBCELLULAR LOCATION: Membrane.
CC -1- TISSUE SPECIFICITY: Heart.
CC -1- PTM: Phosphorylated in response to beta-adrenergic stimulation.
CC -1- SIMILARITY: Belongs to the phospholamban family.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
CC EMBL, M63600; -. NOT ANNOTATED_CDS.
CC DR EMBL; M63601; AAA31445.1; -.
CC DR EMBL; Y00761; CAA68730.1; -.
CC DR PIR; B40424; B40424.
CC DR HSSP; P07473; 1FJK.
CC DR InterPro; IPR005984; P_lamban.
CC DR PIRSF; PIRSF001665; PLB; 1.
CC DR TIGRFAWS; TIGR01294; P_lamban; 1.
CC DR Acetylation; Phosphorylation; Transmembrane.
CC FT DOMAIN 1 31 Cytoplasmic (Potential).
CC FT TRANSMEM 32 52 Potential.
CC FT MOD_RES 1 1 N-acetylmethionine (By similarity).
CC FT MOD_RES 16 16 Phosphoserine (by PKA) (By similarity).
CC FT MOD_RES 17 17 Phosphothreonine (by CamK) (By
similarity).

```



```

RA MEDLINE=955296769; PubMed=7779806;
RX Mortenliehr-Smith R.J., Pitzemberger S.M., Burke C.J., Middaugh C.R.,
RA Garsky V.M., Johnson R.G.,
RA "Solution structure of the cytoplasmic domain of phospholamban:
RT phosphorylation leads to a local perturbation in secondary
RT structure.";
RL Biochemistry 34:7603-7613(1995).
RN [6]
RP 3D-STRUCTURE MODELING.
RX MEDLINE=95269058; PubMed=7749920;
RA Adams P.D., Atkin I.T., Engelman D.M., Bruenger A.T.;
RA "Computational searching and mutagenesis suggest a structure for the
RT pentameric transmembrane domain of phospholamban.";
RL Nat. Struct. Biol. 2:154-162(1995).
RN [7]
RP 3D-STRUCTURE MODELING.
RX MEDLINE=98170970; PubMed=9512019;
RA Herzog P., Hubbard R.E.;
RA "Using experimental information to produce a model of the
RT transmembrane domain of the ion channel phospholamban.";
RL Biophys. J. 74:1203-1214(1998).
CC -1- FUNCTION: Phospholamban has been postulated to regulate the
CC activity of the calcium pump of cardiac sarcoplasmic reticulum.
CC -1- SUBUNIT: Homopentamer.
CC -1- SUBCELLULAR LOCATION: Membrane.
CC -1- TISSUE SPECIFICITY: Heart.
CC -1- PTM: Phosphorylated in response to beta-adrenergic stimulation.
CC -1- SIMILARITY: Belongs to the phospholamban family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL, M63603; AAA60083.1; -.
DR EMBL, M60411; AAA60109.1; -.
DR EMBL, AF177764; AAD55950.1; -.
DR EMBL, BC005269; AAO5269.1; -.
DR PIR, A40424; A40424.
DR PDB, 1K9N; Model; A/B/C/D/E=35-52.
DR PDB, 1KCH; Model; A/B/C/D/E=35-52.
DR PDB, 1PLN; Model; A/B/C/D/E=35-52.
DR PDB, 1PLP; Model; A/B/C/D/E=35-52.
DR PDB, 1PSL; Model; A/B/C/D/E=1-52.
DR GeneW, HGNC:9080; PLN.
DR H-InvDB, HIX006177; -.
DR MIM, 172405; -.
DR InterPro, IPR005984; P_lamban.
DR Pfam, PF04272; Phospholamban; 1.
DR PIRSF, PIRSF01665; PLB; 1.
DR TIGRFAMs, TIGR01294; P_lamban; 1.
KM 3D-structure; Acetylation; Phosphorylation; Transmembrane.
FT DOMAIN 1 31 Cytoplasmic (Potential).
FT TRANSMEM 32 52 N-acetylmethionine (By similarity).
FT MOD_RES 1 1 Phosphoserine (by PKA) (By similarity).
FT MOD_RES 16 16 Phosphothreonine (by CaMK) (By
FT MOD_RES 17 17 similarity).
FT TURN 2 3
FT HELIX 4 14
FT TURN 15 15
SQ SEQUENCE 52 AA; 6108 MW; 0766304A76A854D3 CRC64;
Query Match 96.0%; Score 144; DB 1; Length 52;
Best Local Similarity 96.7%; Pred. No. 6.3e-10;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Cy 1 QARONTLPTNFCILLCILLCILCIYWL 30
Db 23 QARQKLQWLPINFCILLCILLCILCIYWL 52

```

```

RESULT 7
PPLA_CHICK
ID PPLA_CHICK STANDARD; PRT; 52 AA.
AC p26677;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Cardiac phospholamban (PLB).
GN Name:PLN;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauromorpha; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A..
RX MEDLINE=91170195; Pubmed=1825996;
RA Toyofuku T., Zak R.;
RT "Characterization of cDNA and genomic sequences encoding a chicken
RT phospholamban.";
RL J. Biol. Chem. 266:5375-5383(1991).
CC -1 FUNCTION: Phospholamban has been postulated to regulate the
CC activity of the calcium pump of cardiac sarcoplasmic reticulum.
CC -1 SUBUNIT: Homopentamer.
CC -1 SUBCELLULAR LOCATION: Membrane.
CC -1-TISSUE SPECIFICITY: Heart.
CC -1-PMW: Phosphorylated in response to beta-adrenergic stimulation.
CC -1-SIMILARITY: Belongs to the phospholamban family.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC at the European Bioinformatics Institute. There are no restrictions on way
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
-----
DR EMBL; M59039; AAA62738.1; -.
DR EMBL; M59037; -; NOT_ANNOTATED_CDS.
DR EMBL; M59038; AAA63167.1; -.
DR PIR; A39535; A39535.
DR HSSP; P07473; 1FJK.
DR InterPro; IPR005984; P_lamban.
DR Pfam; PF04272; Phospholamban; 1.
DR TRIPSRF; PIRSF001665; PLB; 1.
DR TIGRFAMs; TIGR01294; P_lamban; 1.
KW Acetylation; Phosphorylation; Transmembrane.
FT DOMAIN 1 31 Cytoplasmic (Potentiall).
FT TRANSMEM 32 52 Potential.
FT MOD_RES 1 1 N-acetylmehtionine (by similarity).
FT MOD_RES 16 16 Phosphoserine (by PKA) (By similarity).
FT MOD_RES 17 17 Phosphothreonine (by CaMK) (By
FT similarity).
SQ SEQUENCE 52 AA; 6091 MW; F95F86C36A0CD3B CRC64;
Query Match 91.3%; Score 137; DB 1; Length 52;
Best Local Similarity 90.0%; Pred. No. 4.3e-09;
Matches 27; Conservative 1; Mismatches 2; Indels 0; Gaps 0
Oy 1 QARONLNLFFINFCILLICLLIICLIYWL 30
Db 23 QARQRLQLFLPVNFCLILLICLLIICLIYWL 52
RESULT 8
Q081216 PRELIMINARY; PRT; 792 AA.
AC Q081216;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

```

DE Hypothetical protein PF11605w.
GN Name=PF11605w;
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NC NCB1_TaxID=36329;
RN [1]
RX MEDLINE=2255708; PubMed=1236867; DOI=10.1038/nature01095;
RA Hall N., Pain A., Barriman M., Churcher C., Harris B., Harris D.,
Mungall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K.,
Buckee C.O., Burrows C., Cherevach I., Chillingworth C., Corton C.,
Chillingworth T., Christodoulou Z., Clark L., Clark R., Corcoran C.,
Crosin A., Davies R., Davis P., Dear P., Dearden F., Doggett J.,
Feltwell T., Goble A., Goodhead I., Gilliam R., Hamlin N., Hance Z.,
Hartper D., Hauser H., Hornsby T., Holroyd S., Horrocks P.,
Humphrey S., Jagsels K., James K.D., Johnson D., Kerhornou A.,
Knights A., Kontorov B., Kyes S., Larke N., Lawson D., Lemard N.,
Line A., Maddison M., McLean J., Mooney P., Mould S., Murphy L.,
Oliver K., Ormond D., Price C., Quail M.A., Rabinowitsch E.,
Rajandream M.A., Rutter S., Rutherford K.M., Sanders M., Simmonds M.,
Seeger K., Sharp S., Smith R., Squares R., Squares S., Stevens K.,
Taylor K., Tivey A., Unwin L., Whitehead S., Woodward J.,
RA Sulston J.E., Craig A., Newbold C., Barrell B.G.,
RT "Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13.",
RL Nature 419:527-531(2002).
DR EMBL; AL929359; CAD52007.1; -.
KW Hypothetical protein.
SQ SEQUENCE 792 AA; 96650 MW; 30FF77DBF780C598 CRC64;

Query Match 39.7%; Score 59.5; DB 2; Length 792;
Best Local Similarity 46.2%; Pred. No. 51;
Matches 12; Conservative 7; Mismatches 6; Indels 1; Gaps 1;

Cy 5 NLGNLFINFCLILICLLICITVML 30
Db 710 HMGNLF-NYIFVFCVLIVQIVLIL 734
:::|||||:::|||||:::|||||

RESULT 9
ID Q20783 PRELIMINARY; PRT; 305 AA.
AC Q20783;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein F54E7.5.
GN Name=F54E7.5; ORFNames=F54E7.5;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodertinae; Caenorhabditis.
OX NCB1_TaxID=6239;
RN [1]
RX SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RG MEDLINE=99069613; PubMed=9851916;
RW WormBase Consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RX SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Bentley D.;
RT "The sequence of C. elegans cosmid F54E7.";
RL Submitted (Oct-1994) to the EMBL/Genbank/DBJ databases.
RN [3]
RX SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (Nov-2002) to the EMBL/Genbank/DBJ databases.
RN [4]
RX SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;

RG WormBase Consortium;
RL Submitted (SSP-2004) to the EMBL/Genbank/DBJ databases.
DR EMBL; U00067; AAK20074.1; -.
DR PIR; T34299; T34299.
DR WormBase; WBGene00018828; F54E7.5.
DR WormPep; F54E7.5; CE01316.
KW Hypothetical protein.
SQ SEQUENCE 305 AA; 34300 MW; 0090B966DF621228 CRC64;

Query Match 39.0%; Score 58.5; DB 2; Length 305;
Best Local Similarity 54.2%; Pred. No. 32;
Matches 13; Conservative 3; Mismatches 7; Indels 1; Gaps 1;

Cy 7 QNLFNFCLILICLLICITVML 30
Db 186 QHLFI-ACILILCLTFPCIIIVFI 208
:::|||||:::|||||:::|||||

RESULT 10
ID SARL_MOUSE STANDARD; PRT; 31 AA.
AC Q9C0D6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Sarcolipin.
GN Name=Sin;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCB1_TaxID=10090;
RN [1]
RX SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Stomach, and Tongue;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
Nikaido I., Osato N., Saito R., Suzuki H., Yamana K., Kiyosawa H.,
Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gotojori T.,
Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
Schriml L.M., Kanapin A., Matuda H., Batalov S., Beisel K.W.,
Blake J.A., Brad D., Brusic V., Chochia C., Corbani L.B., Cousins S.,
Dalla E., Dregani T.A., Fletcher C.P., Forrest A., Frazer K.S.,
Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
Nagashima T., Numata K., Okido T., Pavan M.J., Perteu G., Pesole G.,
Petkovsky N., Pillai R., Pontius J.V., Qi D., Ramchandran S.,
Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,
Wilting L.G., Wyrshaw-Boris A., Yangisawa M., Yang I., Yang L.,
Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carlini P., Hayatsu N.,
Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazawa N., Sato K.,
Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda I.,
Hara A., Hashizume W., Imocani K., Ishii Y., Itoh M., Kagawa I.,
Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
Yasunishi A., Yoshino H., Yashizaki Y.;
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [2]
RX SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bernaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Tohhyuki S., Carninci P., Prange C.,
 RA Raha S.S., Locantello N.A., Peters G.J., Abramson R.D., Mullah S.J.,
 RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richardson S., Morley K.C., Hale S., Garcia A.M., Gay L.O., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 CC Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- SUBUNIT: Associated with calcium ATPase SERCA1.
 CC -1- SUBCELLULAR LOCATION: Membrane-associated. Sarcoplasmic reticulum.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AK008863; -; NOT ANNOTATED_CDS.
 CC -----
 DR EMBL; AK008896; BAB25959.1; -;
 DR EMBL; AK009005; BAB26019.1; -;
 DR EMBL; AK009809; BAB26516.1; -;
 DR EMBL; BC028496; AAH28496.1; -;
 DR HSSP; 000631; IJDM.
 DR MGD; MGI:191652; SLN.
 DR InterPro; IPR008028; Sarcoplipin.
 DR Pfam; PF05366; Sarcoplipin; 1.
 DR Sarcoplasmic reticulum; Transmembrane.
 FT TRASNMEM 8 25 Potential.
 FT SEQUENCE 31 AA; 3808 MW; 99310161575EP81D CRC64;
 SQ

Query Match 38.7%; Score 58; DB 1; Length 31;
 Best Local Similarity 45.8%; Pred. No. 6.3;
 Matches 11; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 4 ONLONLFINFCLILCLILCIIV 27
 Db 3 RSTQELFINFVTLVTLVLMILV 26

RESULT 11

Q6SL67 PRELIMINARY; PRT; 31 AA.
 AC Q6SL67;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Sarcoplipin.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Histar; TISSUE=Arctium;
 RA Minamideba S., Yokoyama U., Sato Y., Nakagome M., Mouri M., Uemura N.,
 RA Horii H., Ishikawa Y.,
 RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY456000; AAR19044.1; -;
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0030234; P:enzyme regulator activity; IEA.
 DR InterPro; IPR008028; Sarcoplipin.
 DR Pfam; PF05366; Sarcoplipin; 1.
 SQ SEQUENCE 31 AA; 3808 MW; 99310161575EP81D CRC64;

Query Match 38.7%; Score 58; DB 2; Length 31;
 Best Local Similarity 45.8%; Pred. No. 6.3;
 Matches 11; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 4 ONLONLFINFCLILCLILCIIV 27
 Db 3 RSTQELFINFVTLVTLVLMILV 26

RESULT 12

Q70V94 PRELIMINARY; PRT; 130 AA.
 ID Q70V94;
 AC Q70V94;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE NADH dehydrogenase subunit 1 (fragment).
 GN Name=NADH1;
 OS Cotesia kazak.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Ichneumonidae;
 OC Braconidae; Microgasterinae; Cotesia.
 OX NCBI_TaxID=217438;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Michel-Salzat A., Whitfield J.B.;
 RT "Preliminary evolutionary relationships within the parasitoid wasp
 RT genus Cotesia (Hymenoptera: Braconidae: Microgasterinae): combined
 RT analysis of four molecular markers.";
 RL Syst. Entomol. 29:371-382(2004).
 CC -1- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
 CC -1- SIMILARITY: Belongs to the complex I subunit 1 family.
 DR EMBL; AF535986; CAD59806.1; -;
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR01694; Resp_NADH_dhl.
 DR Pfam; PF00146; NADHdh1; 1.
 DR Mitochondrion; NAD; Oxidoreductase; Transmembrane; Ubiquinone.
 FT NON_TER 1 130
 FT NON_TER 1 130
 FT SEQUENCE 130 AA; 15080 MW; 134A6A937BB37DF5 CRC64;
 SQ

Query Match 38.3%; Score 57.5; DB 2; Length 130;
 Best Local Similarity 53.3%; Pred. No. 22;
 Matches 16; Conservative 2; Mismatches 7; Indels 5; Gaps 1;

QY 5 NLQNL-----FINFCLILCLILCIIVML 29
 Db 96 NLVNLNFKFINFMYPLMLIMISML 125

RESULT 13

Q9PIM9 PRELIMINARY; PRT; 169 AA.
 ID Q9PIM9;
 AC Q9PIM9;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Putative integral membrane protein.
 GN OrderedLocusNames=Cj0266.3, Cj0266c;
 OS Campylobacter jejuni.
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
 OC Campylobacteraceae; Campylobacter.
 OX NCBI_TaxID=197;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NCTC 11168;
 RA MEDLINE=20150912; PubMed=10688204; DOI=10.1038/35001088;
 RA Parthill J., Wren B.W., Mungall K.L., Kettley J.M., Churcher C.M.,
 RA Basham D., Chillingworth T., Davies R.M., Felwell T., Holroyd S.,

```

RA Jagele K., Kariyshev A.V., Moule S., Pallen M.J., Penn C.W.,
RA Quail M.A., Rajadream M.A., Rutherford K.M., van Vliet A.H.M.,
RA Whitehead S., Barrell B.G.;
RT "The genome sequence of the food-borne pathogen Campylobacter jejuni
RT reveals hypervariable sequences."
RL Nature 403:665-668(2000).
DR EMBL; AL139074; CAB2734.1; -.
DR PIR; A81445; A81445.
DR InterPro; IPR010916; TONB_Box_N.
DR PROSITE; PS00430; TONB_DEPENDENT_REC_1; UNKNOWN_1.
KM Complete proteome.
SQ SEQUENCE 169 AA; 19512 MW; E32DF1293031871B CRC64;

Query Match 38.0%; Score 57; DB 2; Length 169;
Best Local Similarity 52.6%; Pred. No. 30;
Matches 10; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 11 INFCLILICLLICLIYML 29
Db 9 IAFILILICPALICLIIFL 27

RESULT 14
Q6V2B7 PRELIMINARY; PRT; 35 AA.
AC Q6V2B7;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE NADH dehydrogenase subunit 1 (Fragment).
OS Bidesodes limestonensis.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Coleoptera; Adephaga; Dytiscidae;
OC Hydroporinae; Bidesodini; Bidesodes.
OX NCBI_TaxID=245104;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14761060;
RA Lays R., Watts C.H.S., Cooper S.J.B., Humphreys W.F.;
RT "Evolution of subterranean diving beetles (Coleoptera: Dytiscidae:
RT Hydrophilini, Bidesodini) in the arid zone of Australasia."
RL Evolution 57:2819-2834(2003).
CC -1- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC -1- SIMILARITY: Belongs to the complex I subunit 1 family.
DE EMBL; AY338827; AAR0201.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
DR InterPro; IPR001694; Resp_NADH_dhl.
DR Pfam; PF00146; NADHdh; 1.
DR Mitochondrion; NAD; Oxidoreductase; Transmembrane; Ubiquinone.
FT NON TER 35
SQ SEQUENCE 35 AA; 4126 MW; 4FBP64DC8EB6F20 CRC64;

Query Match 37.3%; Score 56; DB 2; Length 35;
Best Local Similarity 60.0%; Pred. No. 12;
Matches 12; Conservative 4; Mismatches 2; Indels 2; Gaps 1;

Qy 10 FINFLILICLLILICLIY 27
Db 4 FYDFMLILICLLILVLCV 23

RESULT 15
Q8BS41 PRELIMINARY; PRT; 110 AA.
AC Q8BS41;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Mus musculus adult male aorta and vein cDNA. RIKEN full-length
DE enriched library, clone:R530008A08 product:hypothetical protein, full
DE insert sequence.
OS Mus musculus (Mouse).

```

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning."
RL Mech. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
RA The FANTOM Consortium;
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes."
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Atzawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Kitsuana T., Tashiro H., Itoh M.,
RA Suni N., Ishi Y., Nakamura S., Hazama M., Nishino T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kasai H.,
RA Fujiwara K., Inoue K., Togawa Y., Izawa M., Ohta E., Watahiki K.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer."
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
RA Adachi J., Atzawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Imili Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohashi T., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AK040657; BAC30658.1; -.
KM Hypothetical protein.
SQ SEQUENCE 110 AA; 12777 MW; CBD74D054430317B CRC64;

Query Match 37.3%; Score 56; DB 2; Length 110;
Best Local Similarity 42.9%; Pred. No. 29;
Matches 9; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

Qy 10 FINFLILICLLILICLIYML 30

```


Db 86 PALFCFVLFCLIAKFL 106

Search completed: July 7, 2005, 15:41:08
Job time : 395 secs

This Does Rink (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using ew model

Run on: July 7, 2005, 15:09:35 ; Search time 91 Seconds

(without alignments)
24.610 Million cell updates/sec

Title: US-10-724-532-1

Perfect score: 150

Sequence: 1 QARQNLQNLFINFCLILCLILCLILCLIVMLL 30

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Issued Patents AA:*

- 1: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
- 2: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
- 3: /cgn2_6/prodata/1/1aa/5C_COMB.pep:*
- 4: /cgn2_6/prodata/1/1aa/5D_COMB.pep:*
- 5: /cgn2_6/prodata/1/1aa/5E_COMB.pep:*
- 6: /cgn2_6/prodata/1/1aa/5F_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	150	100.0	52	4	US-09-252-063-3
2	150	100.0	52	4	US-09-252-063-4
3	150	100.0	52	4	US-09-252-063-5
4	150	100.0	52	4	US-09-252-063-6
5	150	100.0	52	4	US-09-549-8728-14
6	150	100.0	52	4	US-09-549-8728-15
7	150	100.0	52	4	US-09-722-440-3
8	150	100.0	52	4	US-09-722-440-4
9	150	100.0	52	4	US-09-722-440-5
10	150	100.0	52	4	US-09-722-440-6
11	144	96.0	52	4	US-09-252-063-1
12	144	96.0	52	4	US-09-252-063-2
13	144	96.0	52	4	US-09-722-440-1
14	144	96.0	52	4	US-09-722-440-2
15	144	96.0	89	4	US-09-949-016-7310
16	137	91.3	52	4	US-09-252-063-7
17	137	91.3	52	4	US-09-722-440-7
18	130	86.7	27	3	US-09-124-671-7
19	130	86.7	90	3	US-09-124-671-25
20	75	50.0	16	4	US-09-491-614B-17
21	69	46.0	36	4	US-09-252-063-9
22	69	46.0	36	4	US-09-722-440-9
23	56.5	37.7	393	4	US-09-248-796A-22604
24	55	36.7	31	4	US-09-949-016-6310
25	54	36.0	503	4	US-09-248-796A-20120
26	53	35.3	101	4	US-09-248-796A-26669
27	53	35.3	236	4	US-09-270-767-41748

28	52	34.7	529	3	US-09-500-063-2	Sequence 2, Appl
29	52	34.7	713	4	US-09-107-532A-4559	Sequence 4559, Ap
30	52	34.7	1182	3	US-09-293-505-7	Sequence 7, Appl
31	52	34.7	1182	4	US-09-060-939A-7	Sequence 7, Appl
32	52	34.7	1203	3	US-09-207-857-2	Sequence 2, Appl
33	52	34.7	1203	3	US-09-293-505-2	Sequence 2, Appl
34	52	34.7	1203	4	US-09-909-280A-2	Sequence 2, Appl
35	52	34.7	1203	4	US-09-060-939A-2	Sequence 2, Appl
36	51	34.0	114	4	US-09-270-767-39797	Sequence 39797, A
37	51	34.0	114	4	US-09-270-767-55014	Sequence 55014, A
38	51	34.0	149	4	US-09-270-767-33296	Sequence 33296, A
39	51	34.0	149	4	US-09-270-767-48513	Sequence 48513, A
40	51	34.0	584	4	US-09-693-746-22	Sequence 22, Appl
41	50.5	33.7	218	4	US-09-134-000C-4489	Sequence 4489, Ap
42	50	33.3	154	3	US-09-193-104-13	Sequence 13, Appl
43	50	33.3	154	3	US-09-193-104-14	Sequence 14, Appl
44	50	33.3	154	3	US-09-193-104-15	Sequence 15, Appl
45	50	33.3	154	3	US-09-193-104-16	Sequence 16, Appl

ALIGNMENTS

```
RESULT 1
US-09-252-063-3
; Sequence 3, Application US/09252063
; Patent No. 6538022
; GENERAL INFORMATION:
; APPLICANT: Pollesello, Piero
; APPLICANT: Ovaska, Martti
; APPLICANT: Tenhunen, Jukka
; APPLICANT: Viidgren, Jukka
; APPLICANT: Yliperttula-Ikonen, Marjo
; APPLICANT: Tilmann, Carola
; APPLICANT: Lotca, Timo
; TITLE OF INVENTION: Compounds for Deactivating Phospholamban Function on
; FILE REFERENCE: 1102.0250001
; CURRENT APPLICATION NUMBER: US/09/252,063
; EARLIER FILING DATE: 1999-02-18
; EARLIER APPLICATION NUMBER: 08/937,117
; EARLIER FILING DATE: 1997-09-24
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Canis sp.
US-09-252-063-3
Query Match          100.0%; Score 150; DB 4; Length 52;
Best Local Similarity 100.0%; Pred.No. 4.4e-13;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 QARQNLQNLFINFCLILCLILCLIVMLL 30
DB      23 QARQNLQNLFINFCLILCLILCLIVMLL 52
RESULT 2
US-09-252-063-4
; Sequence 4, Application US/09252063
; Patent No. 6538022
; GENERAL INFORMATION:
; APPLICANT: Pollesello, Piero
; APPLICANT: Ovaska, Martti
; APPLICANT: Tenhunen, Jukka
; APPLICANT: Viidgren, Jukka
; APPLICANT: Yliperttula-Ikonen, Marjo
; APPLICANT: Tilmann, Carola
; APPLICANT: Lotca, Timo
; APPLICANT: Kaivoala, Juhna
```

;; TITLE OF INVENTION: Compounds for Deactivating Phospholamban Function on
;; TITLE OF INVENTION: Ca-ATPase (Phospholamban Inhibitors)
;; FILE REFERENCE: 1102.0250001
;; CURRENT APPLICATION NUMBER: US/09/252,063
;; CURRENT FILING DATE: 1999-02-18
;; EARLIER APPLICATION NUMBER: 08/937,117
;; EARLIER FILING DATE: 1997-09-24
;; NUMBER OF SEQ ID NOS: 10
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 4
;; LENGTH: 52
;; TYPE: PRT
;; ORGANISM: Oryctolagus cuniculus
US-09-252-063-4

Query Match 100.0%; Score 150; DB 4; Length 52;
Best Local Similarity 100.0%; Pred. No. 4.4e-13;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QARQNLQNLFINFCLILICLLILICIIYVWL 30
Db 23 QARQNLQNLFINFCLILICLLILICIIYVWL 52

RESULT 3
US-09-252-063-5
;; Sequence 5, Application US/09252063
;; Patent No. 6538022
;; GENERAL INFORMATION:
;; APPLICANT: Pollesello, Piero
;; APPLICANT: Ovaska, Martti
;; APPLICANT: Tenhunen, Jukka
;; APPLICANT: Viipertula-Ikonen, Marjo
;; APPLICANT: Tilgmann, Carola
;; APPLICANT: Lotia, Timo
;; TITLE OF INVENTION: Compounds for Deactivating Phospholamban Function on
;; TITLE OF INVENTION: Ca-ATPase (Phospholamban Inhibitors)
;; FILE REFERENCE: 1102.0250001
;; CURRENT APPLICATION NUMBER: US/09/252,063
;; CURRENT FILING DATE: 1999-02-18
;; EARLIER APPLICATION NUMBER: 08/937,117
;; EARLIER FILING DATE: 1997-09-24
;; NUMBER OF SEQ ID NOS: 10
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 5
;; LENGTH: 52
;; TYPE: PRT
;; ORGANISM: Rattus sp.
US-09-252-063-5

Query Match 100.0%; Score 150; DB 4; Length 52;
Best Local Similarity 100.0%; Pred. No. 4.4e-13;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QARQNLQNLFINFCLILICLLILICIIYVWL 30
Db 23 QARQNLQNLFINFCLILICLLILICIIYVWL 52

RESULT 4
US-09-252-063-6
;; Sequence 6, Application US/09252063
;; Patent No. 6538022
;; GENERAL INFORMATION:
;; APPLICANT: Pollesello, Piero
;; APPLICANT: Ovaska, Martti
;; APPLICANT: Tenhunen, Jukka
;; APPLICANT: Viipertula-Ikonen, Marjo
;; APPLICANT: Tilgmann, Carola
;; APPLICANT: Lotia, Timo

;; APPLICANT: Kaivola, Juha
;; TITLE OF INVENTION: Compounds for Deactivating Phospholamban Function on
;; TITLE OF INVENTION: Ca-ATPase (Phospholamban Inhibitors)
;; FILE REFERENCE: 1102.0250001
;; CURRENT APPLICATION NUMBER: US/09/252,063
;; CURRENT FILING DATE: 1999-02-18
;; EARLIER APPLICATION NUMBER: 08/937,117
;; EARLIER FILING DATE: 1997-09-24
;; NUMBER OF SEQ ID NOS: 10
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 6
;; LENGTH: 52
;; TYPE: PRT
;; ORGANISM: Mus sp.
US-09-252-063-6

Query Match 100.0%; Score 150; DB 4; Length 52;
Best Local Similarity 100.0%; Pred. No. 4.4e-13;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QARQNLQNLFINFCLILICLLILICIIYVWL 30
Db 23 QARQNLQNLFINFCLILICLLILICIIYVWL 52

RESULT 5
US-09-549-872B-14
;; Sequence 14, Application US/09549872B
;; Patent No. 6540996
;; GENERAL INFORMATION:
;; APPLICANT: Zwaal, Richard
;; APPLICANT: Groenen, Jose
;; APPLICANT: Bogaert, Thierry
;; TITLE OF INVENTION: COMPOUND SCREENING METHODS
;; FILE REFERENCE: D00590/70008 (JRV/RE)
;; CURRENT APPLICATION NUMBER: US/09/549,872B
;; CURRENT FILING DATE: 2000-04-14
;; PRIOR APPLICATION NUMBER: GB 9908670.4
;; PRIOR FILING DATE: 1999-04-15
;; PRIOR APPLICATION NUMBER: US 60/129,596
;; PRIOR FILING DATE: 1999-04-15
;; PRIOR APPLICATION NUMBER: GB 9912736.7
;; PRIOR FILING DATE: 1999-06-01
;; NUMBER OF SEQ ID NOS: 39
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 14
;; LENGTH: 52
;; TYPE: PRT
;; ORGANISM: Sus sp.
US-09-549-872B-14

Query Match 100.0%; Score 150; DB 4; Length 52;
Best Local Similarity 100.0%; Pred. No. 4.4e-13;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QARQNLQNLFINFCLILICLLILICIIYVWL 30
Db 23 QARQNLQNLFINFCLILICLLILICIIYVWL 52

RESULT 6
US-09-549-872B-15
;; Sequence 15, Application US/09549872B
;; Patent No. 6540996
;; GENERAL INFORMATION:
;; APPLICANT: Zwaal, Richard
;; APPLICANT: Groenen, Jose
;; APPLICANT: Bogaert, Thierry
;; TITLE OF INVENTION: COMPOUND SCREENING METHODS
;; FILE REFERENCE: D00590/70008 (JRV/RE)
;; CURRENT APPLICATION NUMBER: US/09/549,872B
;; CURRENT FILING DATE: 2000-04-14
;; PRIOR APPLICATION NUMBER: GB 9908670.4

```
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: US 60/129,596
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: GB 9912736.7
; PRIOR FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-549-872B-15
```

```
Query Match          100.0%; Score 150; DB 4; Length 52;
Best Local Similarity 100.0%; Pred. No. 4.4e-13;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 QARONLQNFNFCLILICLLICLIIVMLL 30
Db      23 QARONLQNFNFCLILICLLICLIIVMLL 52
```

```
RESULT 7
US-09-722-440-3
; Sequence 3, Application US/09722440
; Patent No. 6774103
```

```
; GENERAL INFORMATION:
; APPLICANT: Pollesello, Piero
; APPLICANT: Ovasaka, Martti
; APPLICANT: Tenhunen, Jukka
; APPLICANT: Vidgren, Jukka
; APPLICANT: Yliperttula-Ikonen, Marjo
; APPLICANT: Tilgmann, Carola
; APPLICANT: Lotte, Timo
; APPLICANT: Kaiyola, Juha
; TITLE OF INVENTION: Compounds for Deactivating Phospholamban Function on
; FILE REFERENCE: 1102.0250001
; CURRENT APPLICATION NUMBER: US/09/722,440
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/252,063
; PRIOR FILING DATE: 1999-02-18
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Canis sp.
US-09-722-440-3
```

```
Query Match          100.0%; Score 150; DB 4; Length 52;
Best Local Similarity 100.0%; Pred. No. 4.4e-13;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 QARONLQNFNFCLILICLLICLIIVMLL 30
Db      23 QARONLQNFNFCLILICLLICLIIVMLL 52
```

```
RESULT 8
US-09-722-440-4
; Sequence 4, Application US/09722440
; Patent No. 6774103
```

```
; GENERAL INFORMATION:
; APPLICANT: Pollesello, Piero
; APPLICANT: Ovasaka, Martti
; APPLICANT: Tenhunen, Jukka
; APPLICANT: Vidgren, Jukka
; APPLICANT: Yliperttula-Ikonen, Marjo
; APPLICANT: Tilgmann, Carola
; APPLICANT: Lotte, Timo
; APPLICANT: Kaiyola, Juha
; TITLE OF INVENTION: Compounds for Deactivating Phospholamban Function on
```

```
; TITLE OF INVENTION: Ca-ATPase (Phospholamban Inhibitors)
; FILE REFERENCE: 1102.0250001
; CURRENT APPLICATION NUMBER: US/09/722,440
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/252,063
; PRIOR FILING DATE: 1999-02-18
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Oryctolagus cuniculus
US-09-722-440-4
```

```
Query Match          100.0%; Score 150; DB 4; Length 52;
Best Local Similarity 100.0%; Pred. No. 4.4e-13;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 QARONLQNFNFCLILICLLICLIIVMLL 30
Db      23 QARONLQNFNFCLILICLLICLIIVMLL 52
```

```
RESULT 9
US-09-722-440-5
; Sequence 5, Application US/09722440
; Patent No. 6774103
```

```
; GENERAL INFORMATION:
; APPLICANT: Pollesello, Piero
; APPLICANT: Ovasaka, Martti
; APPLICANT: Tenhunen, Jukka
; APPLICANT: Vidgren, Jukka
; APPLICANT: Yliperttula-Ikonen, Marjo
; APPLICANT: Tilgmann, Carola
; APPLICANT: Lotte, Timo
; APPLICANT: Kaiyola, Juha
; TITLE OF INVENTION: Compounds for Deactivating Phospholamban Function on
; FILE REFERENCE: 1102.0250001
; CURRENT APPLICATION NUMBER: US/09/722,440
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/252,063
; PRIOR FILING DATE: 1999-02-18
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Rattus sp.
US-09-722-440-5
```

```
Query Match          100.0%; Score 150; DB 4; Length 52;
Best Local Similarity 100.0%; Pred. No. 4.4e-13;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 QARONLQNFNFCLILICLLICLIIVMLL 30
Db      23 QARONLQNFNFCLILICLLICLIIVMLL 52
```

```
RESULT 10
US-09-722-440-6
; Sequence 6, Application US/09722440
; Patent No. 6774103
```

```
; GENERAL INFORMATION:
; APPLICANT: Pollesello, Piero
; APPLICANT: Ovasaka, Martti
; APPLICANT: Tenhunen, Jukka
; APPLICANT: Vidgren, Jukka
; APPLICANT: Yliperttula-Ikonen, Marjo
; APPLICANT: Tilgmann, Carola
; APPLICANT: Lotte, Timo
; APPLICANT: Kaiyola, Juha
```

;; TITLE OF INVENTION: Compounds for Deactivating Phospholamban Function on
;; FILE REFERENCE: 1102.0250001
;; CURRENT APPLICATION NUMBER: US/09/722,440
;; PRIOR FILING DATE: 1997-02-18
;; NUMBER OF SEQ ID NOS: 10
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 6
;; LENGTH: 52
;; TYPE: PRT
;; ORGANISM: Mus sp.
US-09-722-440-6

Query Match 100.0%; Score 150; DB 4; Length 52;
Best Local Similarity 100.0%; Pred. No. 4.4e-13; Indels 0; Gaps 0;
Matches 30; Conservative 0; Mismatches 0;

Qy 1 QARQNLQNLFINFCILICLLICILCIIVML 30
Db 23 QARQNLQNLFINFCILICLLICILCIIVML 52

RESULT 11
US-09-252-063-1
; Sequence 1, Application US/09252063
; Patent No. 6538022
; GENERAL INFORMATION:
; APPLICANT: Pollesello, Piero
; APPLICANT: Ovaska, Martti
; APPLICANT: Tenhunen, Jukka
; APPLICANT: Viigren, Jukka
; APPLICANT: Yliperttula-Ikonen, Marjo
; APPLICANT: Tilgmann, Carola
; APPLICANT: Lotta, Timo
; TITLE OF INVENTION: Compounds for Deactivating Phospholamban Function on
; FILE REFERENCE: 1102.0250001
; CURRENT APPLICATION NUMBER: US/09/252,063
; CURRENT FILING DATE: 1999-02-18
; EARLIER APPLICATION NUMBER: 08/937,117
; PRIOR FILING DATE: 1997-09-24
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-252-063-1

Query Match 96.0%; Score 144; DB 4; Length 52;
Best Local Similarity 96.7%; Pred. No. 2.7e-12; Indels 0; Gaps 0;
Matches 29; Conservative 0; Mismatches 1;

Qy 1 QARQNLQNLFINFCILICLLICILCIIVML 30
Db 23 QARQNLQNLFINFCILICLLICILCIIVML 52

RESULT 12
US-09-252-063-2
; Sequence 2, Application US/09252063
; Patent No. 6538022
; GENERAL INFORMATION:
; APPLICANT: Pollesello, Piero
; APPLICANT: Ovaska, Martti
; APPLICANT: Tenhunen, Jukka
; APPLICANT: Viigren, Jukka
; APPLICANT: Yliperttula-Ikonen, Marjo
; APPLICANT: Tilgmann, Carola
; APPLICANT: Lotta, Timo

;; APPLICANT: Kaivoila, Juha
;; TITLE OF INVENTION: Compounds for Deactivating Phospholamban Function on
;; FILE REFERENCE: 1102.0250001
;; CURRENT APPLICATION NUMBER: US/09/252,063
;; PRIOR FILING DATE: 1999-02-18
;; EARLIER APPLICATION NUMBER: 08/937,117
;; NUMBER OF SEQ ID NOS: 10
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 2
;; LENGTH: 52
;; TYPE: PRT
;; ORGANISM: Sus sp.
US-09-252-063-2

Query Match 96.0%; Score 144; DB 4; Length 52;
Best Local Similarity 96.7%; Pred. No. 2.7e-12; Indels 0; Gaps 0;
Matches 29; Conservative 0; Mismatches 1;

Qy 1 QARQNLQNLFINFCILICLLICILCIIVML 30
Db 23 QARQNLQNLFINFCILICLLICILCIIVML 52

RESULT 13
US-09-722-440-1
; Sequence 1, Application US/09722440
; Patent No. 6774103
; GENERAL INFORMATION:
; APPLICANT: Pollesello, Piero
; APPLICANT: Ovaska, Martti
; APPLICANT: Tenhunen, Jukka
; APPLICANT: Viigren, Jukka
; APPLICANT: Yliperttula-Ikonen, Marjo
; APPLICANT: Tilgmann, Carola
; APPLICANT: Lotta, Timo
; TITLE OF INVENTION: Compounds for Deactivating Phospholamban Function on
; FILE REFERENCE: 1102.0250001
; CURRENT APPLICATION NUMBER: US/09/722,440
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/252,063
; PRIOR FILING DATE: 1999-02-18
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-722-440-1

Query Match 96.0%; Score 144; DB 4; Length 52;
Best Local Similarity 96.7%; Pred. No. 2.7e-12; Indels 0; Gaps 0;
Matches 29; Conservative 0; Mismatches 1;

Qy 1 QARQNLQNLFINFCILICLLICILCIIVML 30
Db 23 QARQNLQNLFINFCILICLLICILCIIVML 52

RESULT 14
US-09-722-440-2
; Sequence 2, Application US/09722440
; Patent No. 6774103
; GENERAL INFORMATION:
; APPLICANT: Pollesello, Piero
; APPLICANT: Ovaska, Martti
; APPLICANT: Tenhunen, Jukka
; APPLICANT: Viigren, Jukka
; APPLICANT: Yliperttula-Ikonen, Marjo
; APPLICANT: Tilgmann, Carola

```

1  APPLICANT: Lotta, Timo
2  APPLICANT: Katvola, Juhna
3  TITLE OF INVENTION: Compounds for Deactivating Phospholamban Function on
4  TITLE OF INVENTION: Ca-ATPase (Phospholamban Inhibitors)
5  FILE REFERENCE: 1102.0250001
6  CURRENT APPLICATION NUMBER: US/09/722,440
7  CURRENT FILING DATE: 2000-11-28
8  PRIOR APPLICATION NUMBER: 09/752,063
9  PRIOR FILING DATE: 1999-02-18
10 NUMBER OF SEQ. ID NOS: 10
11 SOFTWARE: PatentIn Ver. 2.0
12 SEQ ID NO 2
13 LENGTH: 52
14 TYPE: PRT
15 ORGANISM: Sus sp.
16 US-09-722-440-2

```

Query Match	96.0%	Score 144;	DB 4;	Length 52;
Best Local Similarity	96.7%	Pred. No. 2.7e-12;		
Matches 29; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

Qy 1 QARQNQLNLFINFCCLILICLLIICIVMLL 30
 |||||
Dd 23 QARQKLQNLFINFCCLILICLLIICIIVMLL 52

RESULT 15
TIS-09-948

; Sequence 7310, Application US/09949016

; Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE

10 TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
84

FILE REFERENCE: CU001307
CURRENT APPLICATION NUMBER: HC/00/040 015

CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14

; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241

PRIOR APPLICATION NUMBER: 80/241
PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237.768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 73

LENGTH: 89

; TYPE: PRT

ORGANISM: Human

US-09-949-016-7310

Query Match 96.0%; Score 144; DB 4; Length 89;

Best Local Similarity 96.7%; Pred. No. 4.8e-12;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QARQNQLNLFINFCILICILICLLICIIVMLL 30
Db 60 QARQKLQNLFINFCILICILICLLICIIVMLL 89

Search completed: July 7, 2005, 15:44:07
Job time : 91 secs

This Page Blank (uspto)

GENERAL INFORMATION:
APPLICANT: Chien, Kenneth R
APPLICANT: Hoshijima, Masahiko
APPLICANT: Ross, John
APPLICANT: Ikeda, Yasuhiro
TITLE OF INVENTION: HIGH EFFICIENCY CARDIAC GENE TRANSFER
FILE REFERENCE: 6627-PA0123
CURRENT APPLICATION NUMBER: US/09/954,571
PRIORITY FILING DATE: 2001-09-11
PRIORITY APPLICATION NUMBER: 60/231,821
PRIORITY FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.2
SEQ ID NO 3
LENGTH: 52
TYPE: PRT
ORGANISM: Canis familiaris
US-09-954-571-3

Query Match 100.0%; Score 150; DB 9; Length 52;
Best Local Similarity 100.0%; Pred. No. 3,7e-11;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QARQNLQNLFINFCLILICLLICIIIVML 30
Db 23 QARQNLQNLFINFCLILICLLICIIIVML 52

RESULT 3
US-09-954-571-4
Sequence 4, Application US/09954571
Publication No. US20020032167A1
GENERAL INFORMATION:
APPLICANT: Chien, Kenneth R
APPLICANT: Hoshijima, Masahiko
APPLICANT: Ross, John
APPLICANT: Ikeda, Yasuhiro
TITLE OF INVENTION: HIGH EFFICIENCY CARDIAC GENE TRANSFER
FILE REFERENCE: 6627-PA0123
CURRENT APPLICATION NUMBER: US/09/954,571
PRIORITY FILING DATE: 2001-09-11
PRIORITY APPLICATION NUMBER: 60/231,821
PRIORITY FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.2
SEQ ID NO 4
LENGTH: 52
TYPE: PRT
ORGANISM: Mus musculus
US-09-954-571-4

Query Match 100.0%; Score 150; DB 9; Length 52;
Best Local Similarity 100.0%; Pred. No. 3,7e-11;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QARQNLQNLFINFCLILICLLICIIIVML 30
Db 23 QARQNLQNLFINFCLILICLLICIIIVML 52

RESULT 4
US-09-954-571-5
Sequence 5, Application US/09954571
Publication No. US20020032167A1
GENERAL INFORMATION:
APPLICANT: Chien, Kenneth R
APPLICANT: Hoshijima, Masahiko
APPLICANT: Ross, John
APPLICANT: Ikeda, Yasuhiro
TITLE OF INVENTION: HIGH EFFICIENCY CARDIAC GENE TRANSFER
FILE REFERENCE: 6627-PA0123
CURRENT APPLICATION NUMBER: US/09/954,571
PRIORITY FILING DATE: 2001-09-11

PRIORITY APPLICATION NUMBER: 60/231,821
PRIORITY FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.2
SEQ ID NO 5
LENGTH: 52
TYPE: PRT
ORGANISM: Oryctolagus cuniculus
US-09-954-571-5

Query Match 100.0%; Score 150; DB 9; Length 52;
Best Local Similarity 100.0%; Pred. No. 3,7e-11;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QARQNLQNLFINFCLILICLLICIIIVML 30
Db 23 QARQNLQNLFINFCLILICLLICIIIVML 52

RESULT 5
US-10-371-101-14
Sequence 14, Application US/10371101
Publication No. US2003014995A1
GENERAL INFORMATION:
APPLICANT: Zwaal, Richard
APPLICANT: Groenen, Jose
APPLICANT: Bogaert, Thierry
TITLE OF INVENTION: COMPOUND SCREENING METHODS
FILE REFERENCE: D00590.70035-US
CURRENT APPLICATION NUMBER: US/10/371,101
PRIORITY FILING DATE: 2003-02-21
PRIORITY APPLICATION NUMBER: GB 9908670.4
PRIORITY FILING DATE: 1999-04-15
PRIORITY APPLICATION NUMBER: US 60/129,596
PRIORITY FILING DATE: 1999-04-15
PRIORITY APPLICATION NUMBER: GB 9912736.7
PRIORITY FILING DATE: 1999-06-01
PRIORITY APPLICATION NUMBER: 09/549,872
PRIORITY FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 14
LENGTH: 52
TYPE: PRT
ORGANISM: Sus sp.
US-10-371-101-14

Query Match 100.0%; Score 150; DB 14; Length 52;
Best Local Similarity 100.0%; Pred. No. 3,7e-11;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QARQNLQNLFINFCLILICLLICIIIVML 30
Db 23 QARQNLQNLFINFCLILICLLICIIIVML 52

RESULT 6
US-10-371-101-15
Sequence 15, Application US/10371101
Publication No. US2003014995A1
GENERAL INFORMATION:
APPLICANT: Zwaal, Richard
APPLICANT: Groenen, Jose
APPLICANT: Bogaert, Thierry
TITLE OF INVENTION: COMPOUND SCREENING METHODS
FILE REFERENCE: D00590.70035-US
CURRENT APPLICATION NUMBER: US/10/371,101
PRIORITY FILING DATE: 2003-02-21
PRIORITY APPLICATION NUMBER: GB 9908670.4
PRIORITY FILING DATE: 1999-04-15
PRIORITY APPLICATION NUMBER: 60/129,596
PRIORITY FILING DATE: 1999-04-15
PRIORITY APPLICATION NUMBER: GB 9912736.7

```

; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: 09/549,872
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 52
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-371-101-15

Query Match          100.0%; Score 150; DB 14; Length 52;
Best Local Similarity 100.0%; Pred. No. 3.7e-11;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QARONLQNLFINFCLILICLLICITIVMLL 30
DB 23 QARONLQNLFINFCLILICLLICITIVMLL 52

RESULT 7
US-10-760-721-1
; Sequence 1, Application US/10760721
; Publication No. US20040213400A1
; GENERAL INFORMATION:
; APPLICANT: Slovic, Avram M.
; APPLICANT: Summa, Christopher M.
; APPLICANT: Seven, Jeffrey G.
; APPLICANT: Degrado, William F.
; APPLICANT: Kono, Hidetoshi
; TITLE OF INVENTION: Computational Design of a Water-Soluble Analog of a Protein, such
; FILE REFERENCE: 1694.0540001
; CURRENT APPLICATION NUMBER: US/10/760,721
; CURRENT FILING DATE: 2004-01-23
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 53
; TYPE: PRF
; ORGANISM: Canine PUS
US-10-760-721-1

Query Match          100.0%; Score 150; DB 16; Length 53;
Best Local Similarity 100.0%; Pred. No. 3.7e-11;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QARONLQNLFINFCLILICLLICITIVMLL 30
DB 24 QARONLQNLFINFCLILICLLICITIVMLL 53

RESULT 8
US-09-954-571-1
; Sequence 1, Application US/09954571
; Publication No. US20020032167A1
; GENERAL INFORMATION:
; APPLICANT: Chien, Kenneth R.
; APPLICANT: Hoshijima, Maehiko
; APPLICANT: Ross, John
; APPLICANT: Ikeda, Yasuhiro
; TITLE OF INVENTION: HIGH EFFICIENCY CARDIAC GENE TRANSFER
; FILE REFERENCE: 6627-PA0123
; CURRENT APPLICATION NUMBER: US/09/954,571
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: 60/231,821
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 52
; TYPE: PRF
; ORGANISM: Artificial
```

```

; FEATURE:
; OTHER INFORMATION: Mutant form of human protein sequence
US-09-954-571-1

Query Match          96.0%; Score 144; DB 9; Length 52;
Best Local Similarity 96.7%; Pred. No. 2e-10;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QARONLQNLFINFCLILICLLICITIVMLL 30
DB 23 QARONLQNLFINFCLILICLLICITIVMLL 52

RESULT 9
US-09-954-571-2
; Sequence 2, Application US/09954571
; Publication No. US20020032167A1
; GENERAL INFORMATION:
; APPLICANT: Chien, Kenneth R.
; APPLICANT: Hoshijima, Maehiko
; APPLICANT: Ross, John
; APPLICANT: Ikeda, Yasuhiro
; TITLE OF INVENTION: HIGH EFFICIENCY CARDIAC GENE TRANSFER
; FILE REFERENCE: 6627-PA0123
; CURRENT APPLICATION NUMBER: US/09/954,571
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: 60/231,821
; PRIOR FILING DATE: 2000-11-09
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 52
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-954-571-2

Query Match          96.0%; Score 144; DB 9; Length 52;
Best Local Similarity 96.7%; Pred. No. 2e-10;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QARONLQNLFINFCLILICLLICITIVMLL 30
DB 23 QARONLQNLFINFCLILICLLICITIVMLL 52

RESULT 10
US-10-408-765A-478
; Sequence 478, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 478
; LENGTH: 52
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-408-765A-478

Query Match          96.0%; Score 144; DB 16; Length 52;
Best Local Similarity 96.7%; Pred. No. 2e-10;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

Qy	1	QARQNLQNLFINFCILILICLLILCIIVMLL	30
Db	23	QARQKLQNLFINFCILILICLLILCIIVMLL	52

```

RESULT 11
US-10-705-791-1
; Sequence 1, Application US/10705791
; Publication No. US20040121942A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; APPLICANT: Chien, Kenneth
; APPLICANT: Dillmann, Wolfgang
; APPLICANT: Minamisawa, Susanne
; APPLICANT: He, Huaping
; APPLICANT: Hoshijima, Masahiko
; APPLICANT: Meyer, Markus
; APPLICANT: Scott, Christopher
; APPLICANT: Wang, Yibin
; APPLICANT: Silverman, Gregg J.
; TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBEAN ACTIVITY FOR THE TREATMENT
; TITLE OF INVENTION: OF CARDIAC DISEASE
; FILE REFERENCE: 6627-PA9025
; CURRENT APPLICATION NUMBER: US/10/705,791
; CURRENT FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: 60/106,718
; PRIOR FILING DATE: 1998-11-02
; PRIOR APPLICATION NUMBER: PCT/US99/25692
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-705-791-1

```

Query Match	96.0%	Score 144	DB 16	Length 52
Best Local Similarity	96.7%	Pred. No. 2e-10		
Matches 29, Conservative	0	Mismatches 1	Indels 0	Gaps 0

RESULT 12
 US-10-705-791-3
 Sequence 3, Application US/10705791
 Publication No. US20040121942A1
 GENERAL INFORMATION:
 APPLICANT: The Regents of the University of California
 APPLICANT: Chien, Kenneth
 APPLICANT: Dillmann, Wolfgang
 APPLICANT: Minamisawa, Susanne
 APPLICANT: He, Huiqing
 APPLICANT: Hoshijima, Masahiko
 APPLICANT: Meyer, Markus
 APPLICANT: Scott, Christopher
 APPLICANT: Wang, Yibin
 APPLICANT: Silverman, Gregg J.
 TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
 TITLE OF INVENTION: OF CARDIAC DISEASE
 FILE REFERENCE: 6627-PA9025
 CURRENT APPLICATION NUMBER: US/10/705,791
 CURRENT FILING DATE: 2003-11-10
 PRIOR APPLICATION NUMBER: 60/106,718
 PRIOR FILING DATE: 1998-11-02
 PRIOR APPLICATION NUMBER: PCT/US99/25692
 PRIOR FILING DATE: 1999-11-02
 NUMBER OF SEQ ID NOS: 19
 SOFTWARE: PatentIn version 3.2

```

; SEQ ID NO 3
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-705-791-3

```

Query Match	96.0%	Score 144;	DB 16;	Length 52;
Best Local Similarity	96.7%	Pred. No. 2e-10;		
Matches 29; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

```

RESULT 13
US-10-705-791-4
; Sequence 4, Application US/10705791
; Publication No. US20040121942M1
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; APPLICANT: Chien, Kenneth
; APPLICANT: Dillmann, Wolfgang
; APPLICANT: Minamisawa, Susanne
; APPLICANT: He, Huaping
; APPLICANT: Hoshijima, Masahiko
; APPLICANT: Meyer, Markus
; APPLICANT: Scott, Christopher
; APPLICANT: Wang, Yibin
; APPLICANT: Silverman, Gregg J.
; TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
; TITLE OF INVENTION: OF CARDIAC DISEASE
; FILE REFERENCE: 6627-PA9025
; CURRENT APPLICATION NUMBER: US/10/705,791
; CURRENT FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: 60/1106,718
; PRIOR FILING DATE: 1998-11-02
; PRIOR APPLICATION NUMBER: PCT/US99/25692
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 52
; TYPE: prt
; ORGANISM: Homo sapiens
US-10-705-791-4

```

Query Match	96.0%;	Score 144;	DB 16;	Length 52;
Best Local Similarity	96.7%;	Pred. No. 2e-10;		
Matches	29;	Conservative	0;	Mismatches 1;
			Indels	0;
			Gaps	0;

```

1      RESULT 14
2      US-10-705-791-5
3      ; Sequence 5, Application US/10705791
4      ; Publication No. US20040121942A1
5      ; GENERAL INFORMATION:
6      ; APPLICANT: The Regents of the University of California
7      ; APPLICANT: Chien, Kenneth
8      ; APPLICANT: Dillmann, Wolfgang
9      ; APPLICANT: Minamisawa, Susame
10     ; APPLICANT: He, Huaping
11     ; APPLICANT: Hoshijima, Masahiko
12     ; APPLICANT: Meyer, Markus
13     ; APPLICANT: Scott, Christopher
14     ; APPLICANT: Wang, Yibin
15     ; APPLICANT: Silverman, Gregg J.
16     ; TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
17     ; TITLE OF INVENTION: OF CARDIAC DISEASE

```

```

: FILE REFERENCE: 6627-PB9025
: CURRENT APPLICATION NUMBER: US/10/705,792
: CURRENT FILING DATE: 2003-11-10
: PRIOR APPLICATION NUMBER: 60/106,718
: PRIOR FILING DATE: 1998-11-02
: PRIOR APPLICATION NUMBER: PCT/US99/25692
: PRIOR FILING DATE: 1999-11-02
: NUMBER OF SEQ ID NOS: 19
: SOFTWARE: PatentIn version 3.2
: SEQ ID NO 5
: LENGTH: 52
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-705-791-5

```

Query Match	96.0%	Score 144;	DB 16;	Length 52;
Best Local Similarity	96.7%	Pred. No. 2e-10;		
Matches 29; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

```
QY      1 QARQLQNLFINFCLILICLLIIVMLL 30  
       |||||  
DB     23 QARQLQNLFINFCLILICLLIIVMLL 52
```

```

RESULT 15
US-10-705-791-6
Sequence 6, Application US/10705791
Publication No. US20040121942A1
GENERAL INFORMATION:
APPLICANT: The Regents of the University of California
APPLICANT: Chien, Kenneth
APPLICANT: Dillmann, Wolfgang
APPLICANT: Minamisawa, Susanne
APPLICANT: He, Hsiuping
APPLICANT: Hoshijima, Masaaki
APPLICANT: Meyer, Markus
APPLICANT: Scott, Christopher
APPLICANT: Wang, Yibin
APPLICANT: Silverman, Gregg J.
TITLE OF INVENTION: METHOD FOR INHIBITION OF PHOSPHOLAMBAN ACTIVITY FOR THE TREATMENT
TITLE OF INVENTION: OF CARDIAC DISEASE
FILE REFERENCE: 6627-PA9025
CURRENT APPLICATION NUMBER: US/10/705,791
CURRENT FILING DATE: 2003-11-10
PRIOR APPLICATION NUMBER: 60/1106,718
PRIOR FILING DATE: 1998-11-02
PRIOR APPLICATION NUMBER: PCT/US99/25692
PRIOR FILING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn version 3.2
SEQ ID NO 6
LENGTH: 52
TYPE: PRT
ORGANISM: Homo sapiens
US-10-705-791-6

```

Query Match	96.0%;	Score 144;	DB 16;	Length 52;
Best Local Similarity	96.7%;	Pred. No. 2e-10;		
Matches 29; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

OY 1 QARQNLQNLFINFCCLILICLLIICIIVMLL 30
 |||||
Db 23 QARQKLQNLFINFCCLILICLLIICIIVMLL 52

Search completed: July 7, 2005, 16:12:48
Job time : 386 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_p2n model

Run on: July 7, 2005, 15:44:11 ; Search time 8374 Seconds

(without alignments)
173.592 Million cell updates/sec

Title: US-10-724-532-1

Perfect score: 150

Sequence: 1 GARONLQNLFINPCLILCLILCLITVML 30

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 2422767955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODE=frame_p2n.model -DEV=xlh
-O=/cgn2.1/USPTO_spool/US10724533/runat_07072005_100329_19987/app_query.fasta_1.199
-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALLIG=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10724533@cgn_1.1_4200@runat_07072005_100329_19987 -NCPU=6 -ICPU=3
-NO WMAP -LARGESUBSTR -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl.1.*
1: gb_da.*
2: gb_hcg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_scs.*
12: gb_sy.*
13: gb_un.*
14: gb_vl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	150	100.0	159	6	BD247907 Method fo
2	150	100.0	159	6	BD247911 Method fo
3	150	100.0	159	6	AR302003 Sequence
4	150	100.0	159	6	AR302007 Sequence

5	150	100.0	159	6	AX040487	AX040487 Sequence
6 <td>150</td> <td>100.0</td> <td>159</td> <td>6</td> <td>AX040491</td> <td>AX040491 Sequence</td>	150	100.0	159	6	AX040491	AX040491 Sequence
7 <td>150</td> <td>100.0</td> <td>159</td> <td>10</td> <td>S95853</td> <td>S95853 phospholamb</td>	150	100.0	159	10	S95853	S95853 phospholamb
8 <td>150</td> <td>100.0</td> <td>314</td> <td>4</td> <td>AY514751</td> <td>AY514751 Canis fam</td>	150	100.0	314	4	AY514751	AY514751 Canis fam
9 <td>150</td> <td>100.0</td> <td>386</td> <td>10</td> <td>S95849</td> <td>S95849 Rattus sp.</td>	150	100.0	386	10	S95849	S95849 Rattus sp.
10 <td>150</td> <td>100.0</td> <td>648</td> <td>10</td> <td>BC061097</td> <td>BC061097 Mus muscu</td>	150	100.0	648	10	BC061097	BC061097 Mus muscu
11 <td>150</td> <td>100.0</td> <td>701</td> <td>10</td> <td>RNPPLAMB</td> <td>RNPPLAMB</td>	150	100.0	701	10	RNPPLAMB	RNPPLAMB
12 <td>150</td> <td>100.0</td> <td>737</td> <td>4</td> <td>DOCPHL</td> <td>DOCPHL</td>	150	100.0	737	4	DOCPHL	DOCPHL
13 <td>150</td> <td>100.0</td> <td>832</td> <td>4</td> <td>DOCPBLA</td> <td>DOCPBLA</td>	150	100.0	832	4	DOCPBLA	DOCPBLA
14 <td>150</td> <td>100.0</td> <td>832</td> <td>4</td> <td>DOCPBLA</td> <td>DOCPBLA</td>	150	100.0	832	4	DOCPBLA	DOCPBLA
15 <td>150</td> <td>100.0</td> <td>858</td> <td>4</td> <td>RABPHLAM2</td> <td>RABPHLAM2</td>	150	100.0	858	4	RABPHLAM2	RABPHLAM2
16 <td>150</td> <td>100.0</td> <td>940</td> <td>10</td> <td>S64792</td> <td>S64792 phospholamb</td>	150	100.0	940	10	S64792	S64792 phospholamb
17 <td>150</td> <td>100.0</td> <td>1786</td> <td>10</td> <td>RATPHOLA02</td> <td>RATPHOLA02</td>	150	100.0	1786	10	RATPHOLA02	RATPHOLA02
18 <td>150</td> <td>100.0</td> <td>2614</td> <td>4</td> <td>CPEPLX</td> <td>CPEPLX</td>	150	100.0	2614	4	CPEPLX	CPEPLX
19 <td>150</td> <td>100.0</td> <td>2841</td> <td>4</td> <td>OCPEPLX</td> <td>OCPEPLX</td>	150	100.0	2841	4	OCPEPLX	OCPEPLX
20 <td>150</td> <td>100.0</td> <td>79895</td> <td>2</td> <td>AC100317</td> <td>AC100317 Mus muscu</td>	150	100.0	79895	2	AC100317	AC100317 Mus muscu
21 <td>150</td> <td>100.0</td> <td>177018</td> <td>2</td> <td>AC097906</td> <td>AC097906 Rattus no</td>	150	100.0	177018	2	AC097906	AC097906 Rattus no
22 <td>150</td> <td>100.0</td> <td>223728</td> <td>2</td> <td>AC097906</td> <td>AC097906 Rattus no</td>	150	100.0	223728	2	AC097906	AC097906 Rattus no
23 <td>150</td> <td>100.0</td> <td>231910</td> <td>2</td> <td>AC128365</td> <td>AC128365 Rattus no</td>	150	100.0	231910	2	AC128365	AC128365 Rattus no
24 <td>150</td> <td>100.0</td> <td>306</td> <td>6</td> <td>CQ447405</td> <td>CQ447405 Sequence</td>	150	100.0	306	6	CQ447405	CQ447405 Sequence
25 <td>144</td> <td>96.0</td> <td>323</td> <td>9</td> <td>HUMPLAM</td> <td>HUMPLAM</td>	144	96.0	323	9	HUMPLAM	HUMPLAM
26 <td>144</td> <td>96.0</td> <td>480</td> <td>6</td> <td>AX894936</td> <td>AX894936 Sequence</td>	144	96.0	480	6	AX894936	AX894936 Sequence
27 <td>144</td> <td>96.0</td> <td>480</td> <td>6</td> <td>BD030469</td> <td>BD030469 Sequence</td>	144	96.0	480	6	BD030469	BD030469 Sequence
28 <td>144</td> <td>96.0</td> <td>980</td> <td>9</td> <td>HSPLBG2</td> <td>HSPLBG2</td>	144	96.0	980	9	HSPLBG2	HSPLBG2
29 <td>144</td> <td>96.0</td> <td>1635</td> <td>6</td> <td>CQ718671</td> <td>CQ718671 Sequence</td>	144	96.0	1635	6	CQ718671	CQ718671 Sequence
30 <td>144</td> <td>96.0</td> <td>1635</td> <td>6</td> <td>AX329653</td> <td>AX329653 Sequence</td>	144	96.0	1635	6	AX329653	AX329653 Sequence
31 <td>144</td> <td>96.0</td> <td>1635</td> <td>9</td> <td>HUMPLAM</td> <td>HUMPLAM</td>	144	96.0	1635	9	HUMPLAM	HUMPLAM
32 <td>144</td> <td>96.0</td> <td>1691</td> <td>2</td> <td>BC005269</td> <td>BC005269 Homo sapi</td>	144	96.0	1691	2	BC005269	BC005269 Homo sapi
33 <td>144</td> <td>96.0</td> <td>60797</td> <td>2</td> <td>AL355356</td> <td>AL355356 Homo sapi</td>	144	96.0	60797	2	AL355356	AL355356 Homo sapi
34 <td>144</td> <td>96.0</td> <td>66092</td> <td>2</td> <td>AL136974</td> <td>AL136974 Homo sapi</td>	144	96.0	66092	2	AL136974	AL136974 Homo sapi
35 <td>144</td> <td>96.0</td> <td>150290</td> <td>9</td> <td>HS509L4</td> <td>HS509L4</td>	144	96.0	150290	9	HS509L4	HS509L4
36 <td>137</td> <td>91.3</td> <td>3312</td> <td>5</td> <td>CHKPLB</td> <td>CHKPLB</td>	137	91.3	3312	5	CHKPLB	CHKPLB
37 <td>137</td> <td>91.3</td> <td>3423</td> <td>5</td> <td>CHKPLB2</td> <td>CHKPLB2</td>	137	91.3	3423	5	CHKPLB2	CHKPLB2
38 <td>130</td> <td>86.7</td> <td>315</td> <td>6</td> <td>AR121629</td> <td>AR121629 Sequence</td>	130	86.7	315	6	AR121629	AR121629 Sequence
39 <td>122</td> <td>81.3</td> <td>133901</td> <td>5</td> <td>BX537355</td> <td>BX537355 Zebrafish</td>	122	81.3	133901	5	BX537355	BX537355 Zebrafish
40 <td>102</td> <td>68.0</td> <td>130240</td> <td>5</td> <td>BX276081</td> <td>BX276081 Zebrafish</td>	102	68.0	130240	5	BX276081	BX276081 Zebrafish
41 <td>89</td> <td>59.0</td> <td>179556</td> <td>2</td> <td>AC013809</td> <td>AC013809 Homo sapi</td>	89	59.0	179556	2	AC013809	AC013809 Homo sapi
42 <td>77 <td>51.3</td> <td>61679</td> <td>2</td> <td>AC100258</td> <td>AC100258 Mus muscu</td> </td>	77 <td>51.3</td> <td>61679</td> <td>2</td> <td>AC100258</td> <td>AC100258 Mus muscu</td>	51.3	61679	2	AC100258	AC100258 Mus muscu
43 <td>77 <td>51.3</td> <td>156495</td> <td>2</td> <td>AC126083</td> <td>AC126083 Rattus no</td> </td>	77 <td>51.3</td> <td>156495</td> <td>2</td> <td>AC126083</td> <td>AC126083 Rattus no</td>	51.3	156495	2	AC126083	AC126083 Rattus no
44 <td>77 <td>51.3</td> <td>158864</td> <td>10</td> <td>AC127559</td> <td>AC127559 Mus muscu</td> </td>	77 <td>51.3</td> <td>158864</td> <td>10</td> <td>AC127559</td> <td>AC127559 Mus muscu</td>	51.3	158864	10	AC127559	AC127559 Mus muscu
45 <td>77 <td>51.3</td> <td>168515</td> <td>10</td> <td>AC130215</td> <td>AC130215 Mus muscu</td> </td>	77 <td>51.3</td> <td>168515</td> <td>10</td> <td>AC130215</td> <td>AC130215 Mus muscu</td>	51.3	168515	10	AC130215	AC130215 Mus muscu

ALIGNMENTS

RESULT 1	BD247907	159 bp	DNA	linear	PAT 17-JUL-2003
LOCUS	BD247907	Method for screening compounds.			
DEFINITION	BD247907	BD247907.1 GI:33057677			
ACCESSION	BD247907	JP 2002541859-A/9.			
VERSION	BD247907	JP 2002541859-A/9.			
KEYWORDS	BD247907	JP 2002541859-A/9.			
SOURCE	BD247907	JP 2002541859-A/9.			
ORGANISM	BD247907	JP 2002541859-A/9.			
Sus sp.	BD247907	JP 2002541859-A/9.			
REFERENCE	BD247907	JP 2002541859-A/9.			
AUTHORS	BD247907	JP 2002541859-A/9.			
TITLE	BD247907	JP 2002541859-A/9.			
JOURNAL	BD247907	JP 2002541859-A/9.			
COMMENT	BD247907	JP 2002541859-A/9.			
OS	BD247907	JP 2002541859-A/9.			
PN	BD247907	JP 2002541859-A/9.			
PD	BD247907	JP 2002541859-A/9.			
PR	BD247907	JP 2002541859-A/9.			
PI	BD247907	JP 2002541859-A/9.			
PC	BD247907	JP 2002541859-A/9.			
CC	BD247907	JP 2002541859-A/9.			
CH	BD247907	JP 2002541859-A/9.			
FT	BD247907	JP 2002541859-A/9.			

FEATURES
source
Location/Qualifiers
1..159
/organism="Sus sp."
/mol_type="genomic DNA"
/db_xref="taxon:9826"

ORIGIN
Alignment Scores:
Pred. No.: 1.11e-09 Length: 159
Score: 150.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 6

US-10-724-532-1 (1-30) x BD247907 (1-159)

Qy 1 GlnAlaArgGlnAsnLeuGlnAsnLeuPheIleAsnPheCysLeuIleLeuIleCysLeu 20
Db 67 CAGGACGCTCAAAACCTTCAGAACCTATTATCAATTCTGTCTCATCTTATATGCTTC 126

Qy 21 LeuLeuIleCysIleIleValMetLeuLeu 30
Db 127 TTGCTGATTGTCATCATGTCATGCTTCTC 156

RESULT 2
LOCUS BD247911 159 bp DNA linear PAT 17-JUL-2003
DEFINITION Method for screening compounds.
ACCESSION BD247911
VERSION BD247911.1 GI:33057681
KEYWORDS JP 2002541859-A/13.
SOURCE
ORGANISM
other sequences: artificial sequences.
1 (bases 1 to 159)
AUTHORS Zwaal, R., Groenen, J. and Bogaert, T.
TITLE Method for screening compounds
JOURNAL Patent: JP 2002541859-A 13 10-DEC-2002;
DEVGEN NV

COMMENT
OS Artificial Sequence
PN JP 2002541859-A/13
PD 10-DEC-2002
PF 14-APR-2000 JP 2000612503
PR 15-APR-1999 GB 9908670.4, 15-APR-1999 US 60/129596 PR
01-JUN-1999 GB 9912736.7
PI RICHARD ZWAAL, JOSE GROENEN, THIERRY BOGAERT
PC C12Q1/42, C12N15/09, C12Q1/02, C12N15/00
CC Description of Artificial Sequence: HUMANIZED PIG PLB cDNA FH
Key Location/Qualifiers
FT source 1..159
FT /organism='Artificial Sequence'.
FEATURES
source
Location/Qualifiers
1..159
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Alignment Scores:
Pred. No.: 1.11e-09 Length: 159
Score: 150.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 6

US-10-724-532-1 (1-30) x BD247911 (1-159)

Qy 1 GlnAlaArgGlnAsnLeuGlnAsnLeuPheIleAsnPheCysLeuIleLeuIleCysLeu 20
Db 67 CAGGACGCTCAAAACCTTCAGAACCTATTATCAATTCTGTCTCATCTTATATGCTTC 126

Qy 21 LeuLeuIleCysIleIleValMetLeuLeu 30
Db 127 TTGCTGATTGTCATCATGTCATGCTTCTC 156

RESULT 3
LOCUS AR302003 159 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 9 from patent US 6540996.
ACCESSION AR302003
VERSION AR302003.1 GI:31689908
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 159)
AUTHORS Zwaal, R., Groenen, J. and Bogaert, T.
TITLE Compound screening methods
JOURNAL Patent: US 6540996-A 9 01-APR-2003;
FEATURES
source
Location/Qualifiers
1..159
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Alignment Scores:
Pred. No.: 1.11e-09 Length: 159
Score: 150.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 6

US-10-724-532-1 (1-30) x AR302007 (1-159)

Qy 1 GlnAlaArgGlnAsnLeuGlnAsnLeuPheIleAsnPheCysLeuIleLeuIleCysLeu 20
Db 67 CAGGACGCTCAAAACCTTCAGAACCTATTATCAATTCTGTCTCATCTTATATGCTTC 126

Qy 21 LeuLeuIleCysIleIleValMetLeuLeu 30
Db 127 TTGCTGATTGTCATCATGTCATGCTTCTC 156

RESULT 4
LOCUS AR302007 159 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 13 from patent US 6540996.
ACCESSION AR302007
VERSION AR302007.1 GI:31689912
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 159)
AUTHORS Zwaal, R., Groenen, J. and Bogaert, T.
TITLE Compound screening methods
JOURNAL Patent: US 6540996-A 13 01-APR-2003;
FEATURES
source
Location/Qualifiers
1..159
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Alignment Scores:
Pred. No.: 1.11e-09 Length: 159
Score: 150.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 6

US-10-724-532-1 (1-30) x AR302007 (1-159)

Qy 1 GlnAlaArgGlnAsnLeuGlnAsnLeuPheIleAsnPheCysLeuIleLeuIleCysLeu 20

DB 67 CAAGCAGCGCAAAACCTTCAGAACCTATTATCAATTCCTCATCTTAATATGCCCTC 126
QY 21 LeuLeuIleCYeIleIleValMetLeuLeu 30
DB 127 TTGCTGATTGGCATCATCGTGAATGCTTCTC 156

RESULT 5
AX040487 159 bp DNA 1 linear PAT 18-NOV-2000
DEFINITION Sequence 9 from Patent WO0063426.
ACCESSION AX040487
VERSION AX040487.1 GI:11230276
KEYWORDS
SOURCE
ORGANISM Sus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.

REFERENCE 1
AUTHORS Zwaal, R., Groenen, J. and Bogaert, T.
TITLE Compound screening methods
JOURNAL Patent: WO 0063426-A 9 26-OCT-2000;
Devgen NV (BE)

FEATURES
source
1..159
/organism="Sus sp."
/mol_type="unassigned DNA"
/db_xref="taxon:9826"

ORIGIN
Alignment Scores:
Pred. No.: 1,11e-09 Length: 159
Score: 150.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 6

US-10-724-532-1 (1-30) x AX040487 (1-159)

QY 1 GlnAlaArgGlnAsnLeuGlnAsnLeuPheIleAsnPheCysLeuIleLeuIleCysLeu 20
DB 67 CAAGCAGCGCAAAACCTTCAGAACCTATTATCAATTCCTCATCTTAATATGCCCTC 126
QY 21 LeuLeuIleCYeIleIleValMetLeuLeu 30
DB 127 TTGCTGATTGGCATCATCGTGAATGCTTCTC 156

RESULT 6
AX040491 159 bp DNA 1 linear PAT 18-NOV-2000
DEFINITION Sequence 13 from Patent WO0063426.
ACCESSION AX040491
VERSION AX040491.1 GI:11230280
KEYWORDS
SOURCE
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Zwaal, R., Groenen, J. and Bogaert, T.
TITLE Compound screening methods
JOURNAL Patent: WO 0063426-A 13 26-OCT-2000;
Devgen NV (BE)

FEATURES
source
1..159
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="HUMANIZED PIG PLB CDNA"

ORIGIN
Alignment Scores:
Pred. No.: 1,11e-09 Length: 159

Score: 150.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 6

US-10-724-532-1 (1-30) x AX040491 (1-159)

QY 1 GlnAlaArgGlnAsnLeuGlnAsnLeuPheIleAsnPheCysLeuIleLeuIleCysLeu 20
DB 67 CAAGCAGCGCAAAACCTTCAGAACCTATTATCAATTCCTCATCTTAATATGCCCTC 126
QY 21 LeuLeuIleCYeIleIleValMetLeuLeu 30
DB 127 TTGCTGATTGGCATCATCGTGAATGCTTCTC 156

RESULT 7
S95853 159 bp mRNA 1 linear ROD 07-MAY-1993
LOCUS phospholamban [rats, aortic smooth muscle, mRNA, 159 nt].
DEFINITION S95853
ACCESSION S95853
VERSION S95853.1 GI:247932
KEYWORDS
SOURCE
ORGANISM Rattus sp.
Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 159)
AUTHORS Hwang, K.S. and Nadal-Ginard, B.
TITLE Cloning phospholamban cDNA from rat aortic smooth muscle
JOURNAL Adv. Exp. Med. Biol. 304, 387-395 (1991)
MEDLINE 92206263
PubMed 1725098
REMARK Genbank staff at the National Library of Medicine created this
entry [NCBI glibseq 95853] from the original journal article.

FEATURES
source
1..159
/organism="Rattus sp."
/mol_type="mRNA"
/db_xref="taxon:10118"
1..159
/gene="phospholamban, PLN"
1..159
/note="phospholamban, PLN"
/gene="PLN"
/codon_start=1
/product="phospholamban"
/protein_id="AAB21903.1"
/db_xref="GI:247933"
/translation="MEKVQYLRSAIRASSTIEMPOQARQNLQNLFINFCLLICLL
ICIIYML"

ORIGIN
Alignment Scores:
Pred. No.: 1,11e-09 Length: 159
Score: 150.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 10

US-10-724-532-1 (1-30) x S95853 (1-159)

QY 1 GlnAlaArgGlnAsnLeuGlnAsnLeuPheIleAsnPheCysLeuIleLeuIleCysLeu 20
DB 67 CAAGCAGCGCAAAACCTTCAGAACCTATTATCAATTCCTCATCTTAATATGCCCTC 126
QY 21 LeuLeuIleCYeIleIleValMetLeuLeu 30
DB 127 CTGCTGATCTGCATCATCTGATGCTTCTC 156

RESULT 8

AY514751 314 bp DNA linear MAM 02-JUL-2004
 LOCUS AY514751
 DEFINITION Canis familiaris phospholamban (PLN) gene, complete cds.
 ACCESSION AY514751
 VERSION AY514751.1 GI:48476898
 KEYWORDS
 SOURCE
 ORGANISM
 Canis familiaris (dog)
 Canis familiaris
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 REFERENCE
 1 (bases 1 to 314)
 Housley,D.J.E., Ritzert,E. and Venta,P.J.
 Comparative radiation hybrid map of canine chromosome 1
 incorporating SNP and indel polymorphisms
 Genomics 84 (2), 248-264 (2004)
 2 (bases 1 to 314)
 Housley,D.J.E., Ritzert,E. and Venta,P.J.
 Direct Submission
 Submitted (29-DEC-2003) Small Animal Clinical Sciences and
 Microbiology and Molecular Genetics, Michigan State University,
 College of Veterinary Medicine, East Lansing, MI 48824-1314, USA
 FEATURES
 source
 1..314
 /organism="Canis familiaris"
 /mol_type="Genomic DNA"
 /db_xref="taxon:9615"
 /note="Sequence information was obtained from a pool of
 ten breeds: German shepherd dog; Beagle; German shorthair
 pointer; Scottish terrier; Doberman pinscher; Greyhound;
 Siberian husky; Labrador retriever; Collie; Cocker
 spaniel; additional sequence was obtained from a single
 mixed breed dog of unknown origin"
 <1..>314
 /gene="PLN"
 <1..>314
 /gene="PLN"
 /number=2
 <1..39
 /gene="PLN"
 <40..>198
 /gene="PLN"
 /product="phospholamban"
 40..198
 /gene="PLN"
 /codon_start=1
 /product="phospholamban"
 /protein_id="AA044582.1"
 /db_xref="GI:48476898"
 /translation="MDKQYLTTRSAIRASTIEMPOARQNLQNLFINFCILICLL
 ICIIVMLL"
 199..>314
 /gene="PLN"
 ORIGIN
 3' UTR
 Alignment Scores:
 Pred. No.: 2,11e-09 Length: 314
 Score: 150.00 Matches: 30
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 4 Gaps: 0
 US-10-724-532-1 (1-30) x AY514751 (1-314)
 QY 1 GlnAaArgGlnAnLeuGlnAnLeuPheIleAnPheCysLeuIleLeuIleCysLeu 20
 Db 106 CAAGCAGCTCAAAATCTTCAAGACCTATTATTAATTTCTGCTCATTTATATATGCTC 165
 QY 21 LeuLeuIleCysIleIleValMetLeuLeu 30
 Db 166 TTGTTGATCTGCATTCATTTGTATGCTTCTC 195
 RESULT 9

S95849 386 bp mRNA linear ROD 16-DEC-2002
 LOCUS S95849
 DEFINITION Rattus sp. phospholamban (Pln) mRNA, complete cds.
 ACCESSION S95849
 VERSION S95849.1 GI:247934
 KEYWORDS
 SOURCE
 ORGANISM
 Rattus sp.
 Rattus sp.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 REFERENCE
 1 (bases 1 to 386)
 Hwang,K.S. and Nadal-Ginard,B.
 Cloning phospholamban cDNA from rat aortic smooth muscle
 Adv. Exp. Med. Biol. 304, 387-395 (1991)
 JOURNAL MEDLINE 92206263
 PUBMED 1725098
 REMARK
 GenBank staff at the National Library of Medicine created this
 entry [NCBI gi247934 S95849] from the original journal article.
 This sequence comes from Fig.2.
 FEATURES
 source
 1..386
 /organism="Rattus sp."
 /mol_type="mRNA"
 /db_xref="taxon:10118"
 /tissue_type="cardiac smooth muscle"
 1..386
 /gene="Pln"
 159..317
 /gene="PLN"
 /codon_start=1
 /product="phospholamban"
 /protein_id="AA06727.1"
 /db_xref="GI:26986719"
 /translation="MEKQYLTTRSAIRASTIEMPOARQNLQNLFINFCILICLL
 ICIIVMLL"
 ORIGIN
 Alignment Scores:
 Pred. No.: 2,56e-09 Length: 386
 Score: 150.00 Matches: 30
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 10 Gaps: 0
 US-10-724-532-1 (1-30) x S95849 (1-386)
 QY 1 GlnAaArgGlnAnLeuGlnAnLeuPheIleAnPheCysLeuIleLeuIleCysLeu 20
 Db 225 CAAGCGCTCAGAACCTTCAGAACCTTTATCAATTTCTGCTCATTCATATATATGCTG 284
 QY 21 LeuLeuIleCysIleIleValMetLeuLeu 30
 Db 285 CTGCTGATCTGCATTCATTTGTATGCTTCTG 314
 RESULT 10
 BC061097 648 bp mRNA linear ROD 30-JUN-2004
 LOCUS BC061097
 DEFINITION Mus musculus phospholamban, mRNA (cDNA clone MGC:74215
 IMAGE:6772294), complete cds.
 ACCESSION BC061097
 VERSION BC061097.1 GI:38173946
 KEYWORDS
 SOURCE
 ORGANISM
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE
 1 (bases 1 to 648)
 Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
 Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
 Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
 Hopkins,R.F., Jordan,H., Moore,T., Wang,S.I., Wang,J., Hsieh,F.,

Diachenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stappleton, M., Soares, M.B., Bonaldo, M.P., Casavant, T.L., Scherz, T.E., Brownstein, M.J., Uedlin, T.B., Toshiyuki, S., Carlini, P., Prange, C., Rana, S.S., Loquellano, N.A., Peters, G.J., Abrahams, R.D., Mullaly, S.J., Bosak, S.A., McSwan, P.J., McKernan, K.J., Malek, J.A., Gunatane, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulik, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahay, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Snevchenko, Y., Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, Y.S., Krzywinski, M.I., Skliska, V., Small, D.E., Scherch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

2 (bases 1 to 648)
12477932
Strausberg, R.
Direct Submission
Submitted (03-NOV-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Jonathan Kuo, NIMH
cDNA Library Preparation: Michael Brownstein / Ted Uedlin
Laboratory
cDNA library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www-shgc.stanford.edu>
Contact: (Dickson, Mark) mdc@axil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
Series: IRAL Plate: 53 Row: 9 Column: 14
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 12963502.

FEATURES
source
location/Qualifiers
1..648
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="MGC:74215 IMAGE:6772294"
/tissue_type="Testis, mouse"
/clone_lib="NIH_MGC_169"
/lab_host="DH10B"
/note="Vector: pDNR-LIB"
1..648
/gene="pin"
/note="synonym: PLB"
/db_xref="LOCUSID:18821"
/db_xref="MGI:97622"
211..369
/gene="pin"
/codon_start=1
/product="phospholamban"
/protein_id="AAH61097.1"
/db_xref="GI:38173947"
/db_xref="LOCUSID:18821"
/db_xref="MGI:97622"
/translation="MEKVOYLRSAIRASTIEMPOQARONLQNFINCLICLL
ICIIIVML"

ORIGIN
Alignment Scores:
Pred. No.: 4.17e-09 Length: 648

Score: 150.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-724-532-1 (1-30) x BC061097 (1-648)

QY 1 GlnAlaArgGlnAsnLeuGlnAsnLeuPheIleAsnPheCysLeuIleCysLeu 20
277 CAGGACGGCAAACTCCAGAACCATTTATTCGCTCATCTTGATATGCTCG 336

QY 21 LeuLeuIleCysIleIleValMetLeuLeu 30
337 CTGCTGATGTCATCTGTATGCTTCTG 366

RESULT 11
RNPFLAMB 701 bp mRNA linear ROD 09-JUL-1993
LOCUS RNPFLAMB
DEFINITION R.norvegicus mRNA for phospholamban.
ACCESSION X71068
VERSION X71068.1 GI:313809
KEYWORDS phospholamban.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE
AUTHORS 1
TITLE Shanahan, C.M., Weissberg, P.L. and Metcalfe, J.C.
JOURNAL Isolation of gene markers of differentiated and proliferating
MEDLINE vascular smooth muscle cells
PUBMED 93284726
8508530
2 (bases 1 to 701)
AUTHORS Shanahan, C.M.
TITLE Direct Submission
JOURNAL Submitted (26-FEB-1993) C.M. Shanahan, University of Cambridge,
Dept of Biochemistry, Tennis Court Road, Cambridge CB2 1QW, UK

FEATURES
source
location/Qualifiers
1..701
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Wistar"
/db_xref="taxon:10116"
/clone="2RB7"
/tissue_type="aorta smooth muscle"
/clone_lib="lambda-zap"
/dev_stage="adult"
174..332
/codon_start=1
/product="phospholamban"
/protein_id="CAA50394.1"
/db_xref="GI:313810"
/db_xref="GOA:P20006"
/db_xref="UniProt/Swiss-Prot:P20006"
/translation="MEKVOYLRSAIRASTIEMPOQARONLQNFINCLICLL
ICIIIVML"

ORIGIN
Alignment Scores:
Pred. No.: 4.49e-09 Length: 701
Score: 150.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-724-532-1 (1-30) x RNPFLAMB (1-701)

QY 1 GlnAlaArgGlnAsnLeuGlnAsnLeuPheIleAsnPheCysLeuIleCysLeu 20
|||||

Db 240 CAAGCGCTCAGAACCTCCAGAACTCTTTATCAATTCTGTGTCATCTGATATGCTG 299

Qy 21 LeuLeuileCySilelleValMetLeuLeu 30
 |||||
 Db 300 CTGCTGATATGATCATCTGTATGCTCTCTG 329

RESULT 12

SSPUB 737 bp mRNA linear MAM 12-SEP-1993

LOCUS Pig mRNA for phospholamban.

DEFINITION X15075

ACCESSION X15075.1 GI:2055

VERSION calcium regulatory protein; phospholamban; transmembrane protein.

KEYWORDS Sus scrofa (pig)

SOURCE Sus scrofa

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.

REFERENCE 1 (bases 1 to 737)

AUTHORS Verdoomen,H., Wuytsack,F., Eggermont,J.A., De Jaegere,S., Masiën,L., Raeymaekers,L. and Casteels,R.

TITLE cDNA cloning and sequencing of phospholamban from pig stomach smooth muscle

JOURNAL Biochem. J. 262 (1), 353-356 (1989)

MEDLINE 90056437

PUBMED 2530978

REFERENCE 2 (bases 1 to 737)

AUTHORS Eggermont,J.A.

TITLE Direct Submission

JOURNAL Submitted (13-APR-1989) Eggermont J.A., Laboratorium Voor Fysiologie K.U. Leuven, Campus Gasthuisberg O/N, Herestraat 49, B-3000 Leuven, Belgium

COMMENT See <Y00399> for canine phospholamban and <Y00761> for rabbit phospholamban.

FEATURES

source Location/Qualifiers

1..737

/organism="Sus scrofa"

/mol_type="mRNA"

/db_xref="taxon:9823"

/clone="PLB 7"

/tissue_type="smooth muscle"

/clone_lib="lambda gtl1"

/dev_stage="2-day-old piglet"

173..331

/note="unmated protein product; phospholamban (AA 1-52)"

/codon_start=1

/protein_id="CA33171.1"

/db_xref="GI:2056"

/db_xref="GOA:P07473"

/db_xref="UniProt/Swiss-Prot:P07473"

/translation="MDKVQYLTRSAIRRASTIEMPOQARQNLQNLFINFCLILCLLLICIVMLL"

716..721

/note="pot. polyA signal"

737

misc_feature

polyA_site

ORIGIN

Alignment Scores:

Pred. No.: 4.71e-09 Length: 737

Score: 150.00 Matches: 30

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 4 Gaps: 0

US-10-724-532-1 (1-30) x SSPUB (1-737)

Qy 1 GlnAlaArgGlnAsnLeuGlnAsnLeuPheIleAsnPheCysLeuIleLeuIleCysLeu 20
 |||||
 Db 239 CAACGACGTCAAAACCTTCAGAACCTATTATCAATTTCTGTTCATCTTATATGCTC 298

Qy 21 LeuLeuileCySilelleValMetLeuLeu 30

Db 299 TTGCTGATTTGCATCATCGATGATGCTTCTC 328

RESULT 13

DOGPHL 832 bp mRNA linear MAM 27-APR-1993

LOCUS Canine cardiac phospholamban mRNA.

DEFINITION M16012

ACCESSION M16012.1 GI:164043

VERSION phospholamban.

KEYWORDS Canis lupus (gray wolf)

SOURCE Canis lupus

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

REFERENCE 1 (bases 1 to 832)

AUTHORS Fujii,J., Ueno,A., Kitano,K., Tanaka,S., Kadoya,M. and Tada,M.

TITLE Complete complementary DNA-derived amino acid sequence of canine cardiac phospholamban

JOURNAL J. Clin. Invest. 79 (1), 301-304 (1987)

MEDLINE 87083954

PUBMED 3793929

COMMENT Original

FEATURES

source source text: Dog cDNA to mRNA.

location/qualifiers

1..832

/organism="Canis lupus"

/mol_type="mRNA"

/db_xref="taxon:9612"

181..339

/note="cardiac phospholamban"

/codon_start=1

/protein_id="AAA30884.1"

/db_xref="GI:164044"

/translation="MDKVQYLTRSAIRRASTIEMPOQARQNLQNLFINFCLILCLLLICIVMLL"

ORIGIN

Alignment Scores:

Pred. No.: 5.28e-09 Length: 832

Score: 150.00 Matches: 30

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 4 Gaps: 0

US-10-724-532-1 (1-30) x DOGPHL (1-832)

Qy 1 GlnAlaArgGlnAsnLeuGlnAsnLeuPheIleAsnPheCysLeuIleLeuIleCysLeu 20
 |||||
 Db 247 CAACGACGTCAAAACCTTCAGAACCTATTATCAATTTCTGTTCATCTTATATGCTC 306

Qy 21 LeuLeuileCySilelleValMetLeuLeu 30
 |||||
 Db 307 TTGTTGATCTGCATCATCTGTGATGCTTCTC 336

RESULT 14

DOGPHL 832 bp mRNA linear MAM 27-APR-1993

LOCUS Dog cardiac phospholamban mRNA, complete cds.

DEFINITION M35393

ACCESSION M35393.1 GI:164045

VERSION phospholamban.

KEYWORDS Canis sp.

SOURCE Canis sp.

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

REFERENCE 1 (bases 1 to 832)

AUTHORS Uyeda,A., Kitano,K., Fujii,J., Kadoya,M., Tada,M. and Tanaka,S.

TITLE Characterization of recombinant cDNA clones for canine cardiac phospholamban

JOURNAL Nucleic Acids Symp. Ser. 17, 121-124 (1986)

MEDLINE 87174860

PUBMED 3562256

COMMENT Original source text: Dog heart, cDNA to mRNA, clone pPLB1.

FEATURES

source

CDS

ORIGIN

Alignment Scores:

Pred. No.:	5 286-09	Length:	832
Score:	150.00	Matches:	30
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-10-724-532-1 (1-30) x DOGFLBA (1-832)

QY 1 GlnAlaArgGlnAsnLeuGlnAsnLeuPheIleAsnPheCysLeuIleLeuIleCysLeu 20

DB 247 CAAGCAGCTCAAAATCTTCAGAACCTATTATTAATTCTGCTCATTTTATATATGCTC 306

QY 21 LeuLeuIleCysIleIleValMetLeuLeu 30

DB 307 TTGTTGATCTGCATCATCTGATGCTTCTC 336

RESULT 15

RABPHLAM2 858 bp DNA linear MAM 27-APR-1993

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SEGMENT

SOURCE

ORGANISM

Oryctolagus cuniculus (rabbit)

Oryctolagus cuniculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

1 (bases 1 to 858)

Fujii,J., Zarain-Herzberg,A., Willard,H.F., Tada,M. and MacLennan,D.H.

Structure of the rabbit phospholamban gene, cloning of the human cDNA, and assignment of the gene to human chromosome 6

J. Biol. Chem. 266 (18), 11669-11675 (1991)

1828805

COMMENT

FEATURES

source

Original

location text: Rabbit DNA.

location/Qualifiers

1..858

/organism="Oryctolagus cuniculus"

/mol_type="genomic DNA"

/db_xref="taxon:9986"

/tissue_id="rabbit genomic"

join(M63600.1:855..943,428..858)

/product="phospholamban"

428..858

/product="phospholamban"

/number=2

524..682

/function="regulatory protein of sarcoplasmic reticulum Ca-ATPase"

/codon_start=1

/product="phospholamban"

/protein_id="AA31445.1"

/db_xref="GI:165639"

/translation="MEKVOYLRSAIRASTIEMPOARONLQNLFINCLILICLL ICIIVML"

ORIGIN

Alignment Scores:

Pred. No.:	5 436-09	Length:	858
Score:	150.00	Matches:	30
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-10-724-532-1 (1-30) x RABPHLAM2 (1-858)

QY 1 GlnAlaArgGlnAsnLeuGlnAsnLeuPheIleAsnPheCysLeuIleLeuIleCysLeu 20

DB 590 CAAGCAGCTCAAAATCTTCAGAACCTATTATTAATTCTGCTCATTTGATATGCTC 649

QY 21 LeuLeuIleCysIleIleValMetLeuLeu 30

DB 650 CTGCTGATCTGCATCATCTGATGCTTCTC 679

Search completed: July 7, 2005, 18:51:24

Job time : 8380 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: July 7, 2005, 16:04:14 ; Search time 2134 Seconds
(without alignments)
535.112 Million cell updates/sec

Title: US-10-724-532-1
Perfect score: 150
Sequence: 1 QARQLQNLFLNFCILICLLICILVML 30

Scoring table:
BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODE=frame_plus.p2n.model -DEV=xlh
-Q=/cgn2.1/USPTO_spool/US1074532/runat_07072005_100329_19999/app_query.fasta_1.199
-DB=EST -QFMT=fastap -SUPFIX=p2n.rst -MINMATCH=0.1 -LOOFC=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pct -NOM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US1074532@cgn2.1_14352@runat_07072005_100329_19999 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -THREATS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-DEVO TIMEOUT=120 -WARN TIMEOUT=30 -THREATS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*

1:	gb_esc1:*
2:	gb_esc2:*
3:	gb_hic:*
4:	gb_esc3:*
5:	gb_esc4:*
6:	gb_esc5:*
7:	gb_esc6:*
8:	gb_g881:*
9:	gb_g882:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
C 1	150	100.0	179	2	BE113353
2	150	100.0	209	1	AA462116
3	150	100.0	328	1	AA839963
4	150	100.0	331	1	AA655419
5	150	100.0	337	5	BY149365
6	150	100.0	347	1	AA433518
7	150	100.0	359	5	BY068506
8	150	100.0	362	6	BY770786
9	150	100.0	366	1	AI597561

10	150	100.0	369	1	AA499852	AA499852	vg05g01.r
11	150	100.0	373	6	CB041339	CB041339	4003081.B
12	150	100.0	375	5	BY092385	BY092385	BY092385
13	150	100.0	377	2	BF547322	BF547322	UI-R-C2P-
14	150	100.0	378	2	BF044741	BF044741	BP250001B
15	150	100.0	378	5	BY088220	BY088220	BY088220
16	150	100.0	380	5	BY092582	BY092582	BY092582
17	150	100.0	381	5	BK669692	BK669692	BK669692
18	150	100.0	385	5	BY096259	BY096259	BY096259
19	150	100.0	390	1	AI671547	AI671547	AI671547
20	150	100.0	390	1	AA222425	AA222425	MY18805.r
21	150	100.0	402	1	AI554976	AI554976	UI-R-C2P-
22	150	100.0	417	1	AI322542	AI322542	mh89506.Y
23	150	100.0	419	1	AA655212	AA655212	VF13002.X
24	150	100.0	425	1	AI467234	AI467234	VF13002.X
25	150	100.0	432	1	AA432895	AA432895	VF45B05.r
26	150	100.0	432	1	AA422326	AA422326	VF45B05.r
27	150	100.0	434	5	BY456761	BY456761	BY456761
28	150	100.0	437	1	AI322347	AI322347	mc39602.Y
29	150	100.0	439	2	BI115006	BI115006	UI-R-BJ1-
30	150	100.0	442	7	CK332692	CK332692	H8210A04-
31	150	100.0	443	5	BY059966	BY059966	BY059966
32	150	100.0	444	1	AI481388	AI481388	vg12E03.X
33	150	100.0	448	2	AM226892	AM226892	um63B05.Y
34	150	100.0	449	2	BF394968	BF394968	UI-R-CW0-
35	150	100.0	449	2	BE098177	BE098177	UI-R-BJ1-
36	150	100.0	451	4	BI288911	BI288911	UI-R-CS08
37	150	100.0	452	1	AA499951	AA499951	VG06A06.r
38	150	100.0	454	2	BE099930	BE099930	UI-R-BJ1-
39	150	100.0	456	1	AA420262	AA420262	VF51902.r
40	150	100.0	469	1	AA466801	AA466801	vd90611.r
41	150	100.0	476	2	BF525258	BF525258	UI-R-ACO-
42	150	100.0	480	7	CR471116	CR471116	CR471116
43	150	100.0	482	4	BG223610	BG223610	IM0009E08
44	150	100.0	487	4	BG379827	BG379827	UI-R-CS0-
45	150	100.0	490	1	AA435031	AA435031	ve06D10.r

ALIGNMENTS

RESULT 1
BE113353/c 179 bp mRNA linear EST 13-UTR-2000
LOCUS
DEFINITION
UI-R-BJ1-ave-d-04-0-UI-81 UI-R-BJ1 Ratius norvegicus CDNA clone
UI-R-BJ1-ave-d-04-0-UI 3', mRNA sequence.

ACCESSION
BE113353
VERSION
KEYWORDS
SOURCE
ORGANISM
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae;
Rattus.

REFERENCE
1 (bases 1 to 179)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
JOURNAL
MEDLINE
PUBMED
COMMENT
Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Oligo-dT track not found. Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: clones will be available through
Research Genetics (www.resgen.com)
Seq primer: M13 Forward
POLYA=No.

High quality sequence stop: 1

```

ity sequence stop: 1.
Location/Qualifiers
1.209
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:871527"
/sex="male"
/tissue_type="heart"
/dev_stage="4 weeks"
/lab_name="DH10B"
/clone_id="Soares mouse NdyH"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5].
TCTTTCACATCGAATCGAGAGCGCGCGGAATTTTTTTTTTTTTTTTTTT
3.1]; double-stranded cDNA was ligated to Eco RI adaptors
[pharmacia] digested with Not I and cloned into the Not
I and Eco RI sites of the modified pT73 vector. RNA
provided by Dr. Minoru Ko, Wayne State Univ. Library
constructed and normalized by Bento Soares and M. Fatima
Bonaldo."

```

Pred. No.:	5.25e-09	Length:	20
Score:	150.00	Matches:	30
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0

DB: 1 Ga

US-10-724-532-1 (1-30) x AA462116 (1-209)

QY 1 Gln1AargGlnAsnLeuGlnAsnLeuPheLeuIleCysLeu 20

Db	73	CAAGCAGTCAGAACTCTCCAGAACTATTATCAATTCTGCCTCATCTTGATATGCTG	132
Qy	21	LeuLeuIleCysIleIleValMetLeuLeu	30

Db	133	CTGCTGATCTGCATCATTTGNGATCCTTC	162
RESULT 3	110000000	300 bp	-PDM
AA839963			1:10000
			ECM 27, ERM-10000

[illegible]

IMAGE:12599453 Similar (HUMAN) ;, mRNA sequence.

```

VERSION AA839963.1  GI:2916557
KEYWORDS EST.

```

SOURCE ORGANISM	Source
Mus musculus (house mouse)	1
Mus musculus	2
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eumammalia; Theria; Eutheria; Rodentia; Muridae; Mus	3

REFERENCE
AUTHORS
Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Mus.
1 (bases 1 to 328)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.

Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B. and Wilson, D. W. 1998. *Journal of the Royal Society of Medicine* 91: 101-105.

Therising, B., Wylie, L., Lennon, G.
Waterston, R.
The Washington Monument East Project

Unpublished (1996)

CONTACT: MARIA M. MOUSE DSI PROJECT
WASHU-HHMI MOUSE EST PROJECT
 Washington University School of Medicine

4444 Forest Park
Tel: 314 286 1800

Tel: 314 286 1810
 Fax: 314 286 1810
 Email: mousseest@watson.wustl.edu

This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.

Db 269 CTGCTGATTCATCATTCATTCATTCG 298

RESULT 7
BY068506 359 bp mRNA linear EST 06-DEC-2002

LOCUS BY068506
musculus cDNA clone 1920060111 5', mRNA sequence.

ACCESSION
BY068506
EST.
GI:26171725

SOURCE
Mus musculus (house mouse)

ORGANISM
Mus musculus

REFERENCE
AUTHORS
Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamana, I.,
Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
Schonbach, C., Gojobori, T., Balarelli, R., Hill, D. P., Bull, C.,
Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H.,
Batalov, S., Beisel, K. W., Blake, J. A., Brad, D., Bruscia, V.,
Chochia, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A.,
Fletcher, C. P., Forrester, A., Frazer, K. S., Gaasterland, T.,
Gardiner, S., Gissi, C., Godzik, A., Gough, J., Givimond, S.,
Guerin, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A.,
Kawaji, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Konagaya, A.,
Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R.,
Malaite, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,
Numata, K., Okido, T., Pavan, W. J., Petosa, G., Pesole, G.,
Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S.,
Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M.,
Sundin, A., Schneider, C., Semp, C. A., Setou, M., Shimada, K.,
Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M.,
Verardo, R., Wagner, L., Wahlstedt, C., Wang, Y., Watanabe, Y.,
Wells, C., Wilming, L. G., Wymshaw-Boris, A., Yanagisawa, M., Yang, I.,
Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,
Hayatsu, N., Hirozane-Kishikawa, T., Kono, H., Nakamura, M.,
Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
Arakawa, T., Fukuda, S., Hara, A., Hashikume, W., Imotani, K., Ishii, Y.,
Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,
Shinagawa, A., Yaeunishi, A., Yoshino, M., Waterston, R., Lander, E. S.,
Rogers, J., Birney, E. and Hayashizaki, Y.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

JOURNAL
MEDLINE
PUBMED
22354683
12466851

TITLE
CONTACT: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9226
Email: genome-res@gscc.riken.jp, URL: http://genome.gsc.riken.jp/
Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,
Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Kono, H.,
Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Nunahara, R.,
Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,
Shiraki, T., Tagami, M., Waki, K., Watanabe, A., Muramatsu, M. and
Hayashizaki, Y. Direct Submision
Computational Analysis of Full-length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome

Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.

FEATURES
source
Location/Qualifiers
1..359
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="1920060111"
/tissue_type="heart"
/dev_stage="17 days embryo"
/clone_11b="RIKEN full-length enriched, 17 days embryo
heart"

ORIGIN
Alignment Scores:
Pred. No.: 9,336-09 Length: 359
Score: 150.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0

US-10-724-532-1 (1-30) x BY068506 (1-359)

Qy 1 G1A1AATGAG1AAnLeuG1AAnLeuPhe1AAnPheCysLeu1Leu1Leu1CysLeu 20
236 CAAAGCAGCGCAGAAATCTCCAGAACTATTCATTCATTCGCTGATTCGTCG 295

Db 21 Leu1Leu1Cys1Leu1Leu1Val1MetLeu1Leu 30
296 CTGCTGATTCATCATTCATTCATTCGCTTCG 325

Qy 362 bp mRNA linear EST 23-MAR-2004
BY770786
BY770786 RIKEN full-length enriched, 17.5 days embryo whole body
Mus musculus cDNA clone L930045G09 5', mRNA sequence.

LOCUS BY770786
DEFINITION
ACCESSION
BY770786
VERSION
BY770786.1 GI:39695776
KEYWORDS
SOURCE
Mus musculus (house mouse)

ORGANISM
Mus musculus

REFERENCE
AUTHORS
Carninci, P., Waki, K., Shiraki, T., Kono, H., Shibata, K., Itoh, M.,
Aizawa, K., Arakawa, T., Ishii, Y., Sasaki, D., Bono, H., Kondo, S.,
Sugahara, Y., Saito, R., Osato, N., Fukuda, S., Sato, K., Watanabe, A.,
Hirozane-Kishikawa, T., Nakamura, M., Shibata, Y., Yasunishi, A.,
Kikuchi, N., Yoshiki, A., Kusakabe, M., Guadincich, S., Beisel, K.,
Pavan, W., Aldinis, V., Nakagawa, A., Heid, W. A., Iwata, H., Kono, T.,
Nakachi, T. H., Lyons, P., Wells, C., Hume, D. A., Fagiolini, M.,
Hensch, K. K., Brinkmeier, M., Camper, S., Hirota, J., Mombaerts, P.,
Muramatsu, M., Okazaki, Y., Kawai, U. and Hayashizaki, Y.
Targeting a complex transcriptome: the construction of the mouse
full-length cDNA encyclopedia
Genome Res. 13 (6B), 1273-1289 (2003)

JOURNAL
MEDLINE
PUBMED
12819125

TITLE
CONTACT: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gscc.riken.jp, URL: http://genome.gsc.riken.jp/
cDNA library was prepared and sequenced in Mouse Genome

source

1. .369

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="IMAGE:860496"

/sex="male"

/tissue_type="heart"

/dev_stage="4 weeks"

/lab_host="DH10B"

/clone_1lb="Soares mouse NBMH"

/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Alignment Scores:

Pred. No.: 9,61e-09 Length: 369

Score: 150.00 Matches: 30

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 1 Gaps: 0

US-10-724-532-1 (1-30) x AA499852 (1-369)

QY 1 GlnAaAgGlnAnLeuGlnAnLeuPheIleAnPheCysLeuIleLeuIleCysLeu 20

DB 205 CAAGCAGCGTCAAGATCTCCAGAACCTATTATCAATTCCTCCTCATTTGATATGCTCG 264

QY 21 LeuLeuIleCysIleIleValMetLeuLeu 30

DB 265 CTGCTGATCTGCATCTGATGATGCTTCG 294

RESULT 11

CB041339 373 bp mRNA linear EST 15-JAN-2003

LOCUS 4003081 BARC-EMBRAPA 312BOV Bos indicus cDNA clone 312BOV_1A09

DEFINITION Unknown, mRNA sequence.

ACCESSION CB041339

VERSION CB041339.1 GI:27760584

KEYWORDS EST.

SOURCE Bos indicus (zebu)

ORGANISM Bos indicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

1 (bases 1 to 373)

da Mota,A.F., Sonstegard,T.S., Van Tassell,C.P., Matukumalli,L.K., Wood,D.U., Capuco,A.V., Brito,M.A.P., Martinez,M.L., Connor,E.E., Machado,M.A. and Coutinho,L.L.

Construction and Characterization of cDNA Libraries Generated from Mammary Gland Tissues of Holstein (Bos taurus) and Gir (Bos indicus) Cattle

Unpublished (2002)

Contact: Adilson F. da Mota

Gene Evaluation and Mapping Laboratory

USDA, ARS, Animal and Natural Resources Institute

Bldg. 200 Rm3 BARC-East, Beltsville, MD 20705, USA

Tel: 3015048456

Fax: 3015048414

Email: amocae@nrgj.embrrapa.br

Single pass sequencing. Bases called and trimmed with phred 0.000925 using options -trim_alt '-trim_fast. Vector identified by cross match using options -mismatch 12 -minscore 12 PCR Primers

FORWARD: GTTTCACGTCACGACGTTG

BACKWARD: TGACCGATACAAATTCACACAG

Place: 1 row: A column: 09

Seq primer: GTTTCACGTCACGACGTTG

High quality sequence stop: 373.

Location/Qualifiers

source

1. .373

/organism="Bos indicus"

/mol_type="mRNA"

/strain="Brazilian Dairy Gir"

/db_xref="taxon:9915"

/clone="312BOV_1A09"

/sex="female"

/tissue_type="teat claster and alveoli"

/cell_type="multiple"

/dev_stage="involved"

/lab_host="K-12"

/clone_1lb="BARC-EMBRAPA 312BOV"

/note="Organ: mammary; Vector: pUC19; Site 1: SmaI; Site 2: SmaI; This mammary-derived cDNA library was created as part of a collaborative project between the ARS Gene Evaluation and Mapping Laboratory and the EMBRAPA Dairy Cattle Research Center under the sponsorship of USDA, ARS/EMBRAPA-LABEX program in animal genomics. RNA extracted on 6/8/02 with Invitrogen Superscript II at 37 deg C annealing temperature."

ORIGIN

Alignment Scores:

Pred. No.: 9,72e-09 Length: 373

Score: 150.00 Matches: 30

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0

US-10-724-532-1 (1-30) x CB041339 (1-373)

QY 1 GlnAaAgGlnAnLeuGlnAnLeuPheIleAnPheCysLeuIleLeuIleCysLeu 20

DB 111 CAAGCAGCGTCAAAATCTCCAGAACCTATTATCAATTCCTCCTCATTTAATATGCTTC 170

QY 21 LeuLeuIleCysIleIleValMetLeuLeu 30

DB 171 TTGCTGATCTGCATCTGATGATGCTTC 200

RESULT 12

BY092385 375 bp mRNA linear EST 07-DEC-2002

LOCUS BY092385

DEFINITION BY092385 RIKEN full-length enriched, 10 days neonate heart Mus musculus cDNA clone K630091G17 5', mRNA sequence.

ACCESSION BY092385

VERSION BY092385.1 GI:26204485

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 375)

Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Oato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bulc,C., Hume,D.A., Quackenbush,J., Schiml,L.M., Kanapin,A., Mateuda,H., Batilov,S., Beisel,K.W., Blake,J.A., Brdick,D., Brusick,V., Chochois,C., Corbani,L.E., Cousins,S., Della,E., Dregani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gasteierland,T., Gariboldi,M., Giesi,C., Godzik,A., Gough,J., Grimond,S., Guerinich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglocz,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Perlea,G., Pesole,G.,

Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringard, M., Sandelin, A., Schneider, C., Sempke, C. A., Setou, M., Shinada, K., Sultana, R., Tanaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M., Verdado, R., Wagner, L., Wahlstedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L. G., Wyshaw-Boris, A., Yangisawa, M., Yang, I., Yang, L., Yuan, Z., Zavalan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hitozane-Kishikawa, T., Kono, H., Nakamura, M., Sakakume, N., Sato, K., Shiraki, T., Waki, K., Kawai, T., Akazawa, T., Fukuda, S., Hara, A., Hashiura, M., Imotani, K., Ichii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sekai, K., Sasaki, D., Shibata, K., Shingawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S., Rogers, J., Birney, E. and Hayashino, Y.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

COMMENT **Contact:** Yoshihide Hayaahizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222

ORIGIN

Alignment Scores:	
Pred. No.:	9,78e-09
Score:	150.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	5
Length:	375
Matches:	30
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-10-724-532-1 (1-30) x BY092385 (1-375)

ORIGIN

Alignment Scores:

Pred. No.:	9.83e-09	Length:	377
Score:	150.00	Matches:	30
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	2	Gaps:	0

US-10-724-532-1 (1-30) x BF547322 (1-377)

Qy 1 glna1aarglnanleuaglnanleupheilaenphecysleuileuileucysleu 20

Db 41 CAAGCGCGTCCAGAACTCCAGAACTTTATTCATTTCTGCTCATCTTGATATGCTC 100

Qy 21 LeuLeuileuileuileuileuileuileuileuileuileuileuileuileu 30

Db 101 CTGCTGATCTGCATCATCTGATGCTTCTC 130

RESULT 14

BF044741

LOCUS BP250001B10F7 Soares normalized bovine placenta Bos taurus CDNA 378 bp mRNA linear EST 10-OCT-2000

DEFINITION clone BP250001B10F7 5', mRNA sequence.

ACCESSION BF044741

VERSION BF044741.1 GI:10761796

KEYWORDS EST.

SOURCE Bos taurus (cow)

ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

Bovinae; Bos

1 (bases 1 to 378)

Lewin,H.A., Soares,M.B., Rebelz,M., Pardinae,J., Liu,L. and

Larson,J.H.

Bovine ESTs

Unpublished (2000)

Contact: Lewin, H. A.

M. M. Keck Center for Comparative and Functional Genomics

University of Illinois at Urbana-Champaign

340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL

61801, USA

Tel: 217 333 5998

Fax: 217 244 5617

Email: h-lewin@uiuc.edu

Funding for cattle EST sequencing was provided by the USDA National

Research Initiative, Animal Genome Resource Grant AG 99-3205-8534

to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED

from Washington University Genome Center. Vector Trim: 9

Cross-match from Washington University Genome Center PHRAP suite.

This sequence is vector free and at least 200 bp in length.

PCR Primers

FORWARD: TATACGACTCCTATAGG

BACKWARD: ATTAACCTCCTAAG

Insert length: 378 Std Error: 0.00

Plate: BP250001B10 row: F column: 7

Seq primer: AGCGATACCAATTTCACACAGA

High quality sequence step: 378.

Location/Qualifiers

FEATURES

source

1. 378

/organism="Bos taurus"

/mol_type="mRNA"

/db_xref="taxon:9913"

/clone="BP250001B10F7"

/sex="female"

/lab_host="DH10B"

/clone_1b="Soares normalized bovine placenta"

/note="Organ: placenta; Vector: pT733pc; Site: 1; EcorI;

Site_2: NotI; The cDNA library was contributed by the

Soares laboratory and it was constructed and normalized

as described by Bonaldo, M.F., Lennon, G. and Soares,

M.B. (1996), Genome Research 6(9): 791-806. "

ORIGIN

Alignment Scores:

Pred. No.:	9.86e-09	Length:	378
Score:	150.00	Matches:	30
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	2	Gaps:	0

US-10-724-532-1 (1-30) x BF044741 (1-378)

Qy 1 glna1aarglnanleuaglnanleupheilaenphecysleuileuileucysleu 20

Db 235 CAAGACGTCAGAACTCCAGAACTTTATTCATTTCTGCTCATCTTGATATGCTC 294

Qy 21 LeuLeuileuileuileuileuileuileuileuileuileuileuileuileu 30

Db 295 TTGCTGATCTGCATCATCTGATGCTTCTC 324

RESULT 15

BY088220

LOCUS BY088220 RIKEN full-length enriched, 10 days neonate heart Mus 378 bp mRNA linear EST 07-DEC-2002

DEFINITION musculus CDNA clone K630069J15 5', mRNA sequence.

ACCESSION BY088220

VERSION BY088220.1 GI:26203986

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 378)

Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,

Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamana,I.,

Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,

Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bule,C.,

Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matzuda,H.,

Batalov,S., Betzel,K.W., Blake,J.A., Brdt,D., Brusic,V.,

Chorhii,C., Corbani,L.E., Cousine,S., Dalla,E., Dragani,T.A.,

Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,

Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Gilmond,S.,

Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,

Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konegaya,A.,

Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,

Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,

Numata,K., Okido,T., Pavan,W.J., Petrea,G., Pesole,G.,

Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramchandran,S.,

Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,

Sandelin,A., Schneider,C., Sempile,C.A., Secou,M., Shimada,K.,

Sultana,R., Takekura,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,

Veraido,R., Wagner,L., Wallestedt,C., Wang,Y., Watanabe,Y.,

Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,

Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,

Hayatsu,N., Hirozane-Kitahara,T., Kono,H., Nakamura,M.,

Sakazume,N., Sato,K., Shiraki,T., Maki,K., Kawai,J., Aizawa,K.,

Aizawa,T., Fukuda,S., Hara,A., Hashizume,W., Imocani,K., Ishii,Y.,

Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Saeki,D., Shibata,K.,

Shinagawa,A., Yaunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,

Rogers,J., Birney,E. and Hayashizaki,Y.

Analysis of the mouse transcriptome based on functional annotation

of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

Nature 420, 563-573 (2002)

22354683

12466851

JOURNAL MEDLINE PUBMED

COMMENT

Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic

Sciences Center (GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suenho-cho, Tsunumi-ku, Yokohama, Kanagawa 220-0045, Japan

Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: July 7, 2005, 16:06:22 ; Search time 511 Seconds
(without alignments)
96.063 Million cell updates/sec

Title: US-10-724-532-1
Perfect score: 150
Sequence: 1 QARONQNFNFICLLICLLICIIYMLL 30

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 segs, 818138359 residues
Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n model -DRV=rlh
-Q/cgn2_1/USFTO.spool/US10724532/runat_07072005_100330_20013/app_query.fasta_1.199
-DB=Issued_Patents_NA -QFMT=Isaetap -SUFFIX=p2n.rn1 -MINMATCH=0.1 -LOOPL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pcc -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=nt -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10724532 @CNCN 1.1 177 @runat_07072005_100330_20013 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEBUTERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DRV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents NA:*
1: /cgn2_6/prodata/1/ina/5A_COMB.seq.*
2: /cgn2_6/prodata/1/ina/5B_COMB.seq.*
3: /cgn2_6/prodata/1/ina/6A_COMB.seq.*
4: /cgn2_6/prodata/1/ina/6B_COMB.seq.*
5: /cgn2_6/prodata/1/ina/PCTUS_COMB.seq.*
6: /cgn2_6/prodata/1/ina/backfillseq.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	150	100.0	159	4 US-09-549-872B-9	Sequence 9, Appl
2	150	100.0	159	4 US-09-549-872B-13	Sequence 13, Appl
3	144	96.0	480	4 US-09-513-999C-10799	Sequence 10799, A
4	144	96.0	1635	4 US-09-949-016-1439	Sequence 1439, Ap
5	144	96.0	16062	4 US-09-949-016-13181	Sequence 13181, A
6	130	86.7	315	4 US-09-124-671-26	Sequence 26, Appl
7	71	47.3	69764	4 US-09-949-016-15638	Sequence 15638, A
8	68	45.3	490	4 US-09-270-767-10524	Sequence 10524, A
9	68	45.3	553	4 US-09-270-767-11139	Sequence 11139, A
10	68	45.3	992	4 US-09-270-767-14599	Sequence 14599, A
11	66	44.0	93920	4 US-09-949-016-12461	Sequence 12461, A
12	66	44.0	93920	4 US-09-949-016-16853	Sequence 16853, A

C 13	64	42.7	601	4	US-09-949-016-136216	Sequence 136216, A
C 14	64	42.7	58356	4	US-09-949-016-15563	Sequence 15563, A
C 15	63	42.0	202001	4	US-09-734-674-3	Sequence 3, Appl
C 16	62.5	41.7	761	1	US-08-477-877B-83	Sequence 83, Appl
C 17	62.5	41.7	761	1	US-08-472-281A-83	Sequence 83, Appl
C 18	62.5	41.7	761	2	US-08-477-989B-83	Sequence 83, Appl
C 19	62.5	41.7	807	1	US-08-472-281A-90	Sequence 90, Appl
C 20	62.5	41.7	807	1	US-08-477-989B-90	Sequence 90, Appl
C 21	62.5	41.7	807	2	US-08-477-989B-90	Sequence 90, Appl
C 22	61	40.7	601	4	US-09-949-016-189393	Sequence 189393, A
C 23	61	40.7	48691	4	US-09-949-016-16308	Sequence 16308, A
C 24	61	40.7	77681	4	US-09-949-016-12770	Sequence 12770, A
C 25	61	40.7	77663	4	US-09-949-016-13751	Sequence 13751, A
C 26	61	40.7	92074	4	US-09-949-016-17163	Sequence 17163, A
C 27	60	40.0	601	4	US-09-949-016-27259	Sequence 27259, A
C 28	60	40.0	601	4	US-09-949-016-27260	Sequence 27260, A
C 29	60	40.0	601	4	US-09-949-016-124818	Sequence 124818, A
C 30	60	40.0	601	4	US-09-949-016-160783	Sequence 160783, A
C 31	60	40.0	601	4	US-09-949-016-160784	Sequence 160784, A
C 32	60	40.0	601	4	US-09-949-016-200644	Sequence 200644, A
C 33	60	40.0	601	4	US-09-949-016-200790	Sequence 200790, A
C 34	60	40.0	12191	4	US-09-949-016-16237	Sequence 16237, A
C 35	60	40.0	25401	4	US-09-949-016-13345	Sequence 13345, A
C 36	60	40.0	32594	4	US-09-949-016-12719	Sequence 12719, A
C 37	60	40.0	32658	4	US-09-949-016-16242	Sequence 16242, A
C 38	60	40.0	152582	4	US-09-949-016-12086	Sequence 12086, A
C 39	60	40.0	152583	4	US-09-949-016-17390	Sequence 17390, A
C 40	60	40.0	152583	4	US-09-949-016-17391	Sequence 17391, A
C 41	60	40.0	183112	4	US-09-949-016-14184	Sequence 14184, A
C 42	60	40.0	192302	4	US-09-949-016-15470	Sequence 15470, A
C 43	59	39.3	1113	4	US-09-248-796A-7619	Sequence 7619, Ap
C 44	59	39.3	1454	4	US-09-270-767-29847	Sequence 29847, A
C 45	59	39.3	2165	2	US-08-263-911-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-09-549-872B-9
Sequence 9, Application US/09549872B

Patent No. 6540996
GENERAL INFORMATION:
APPLICANT: Zwaal, Richard
APPLICANT: Groenen, Jose
APPLICANT: Bogaert, Thierry
TITLE OF INVENTION: COMPOUND SCREENING METHODS
FILE REFERENCE: D00590/70008 (JRV/RE)
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: US/09/549,872B
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: US 60/129,596
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: GB 9912736.7
PRIOR FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 9
LENGTH: 159
TYPE: DNA
ORGANISM: Sus sp.
US-09-549-872B-9

Alignment Scores:

Pred. No.: 4.89e-12
Score: 150.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 4
Length: 159
Matches: 30
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

US-10-724-532-1 (1-30) x US-09-549-872B-9 (1-159)

```
Qy 1 GlnAlaArgGlnAsnLeuGlnAsnLeuPheIleAsnPheCysLeuIleLeuIleCysLeu 20
Db 67 CAAGCAGCTCAAAAGCTTCAGAACTATTATCAATTTCTGTCTCATCTTAATATGCTTC 126
Qy 21 LeuLeuIleCysIleIleValMetLeu 30
Db 127 TTGCTGATTGTCATCATCGTATGCTTCTC 156

RESULT 2
US-09-549-872B-13
; Sequence 13, Application US/09549872B
; Patent No. 6540996
; GENERAL INFORMATION:
; APPLICANT: Zwaal, Richard
; APPLICANT: Groenen, Jose
; APPLICANT: Bogaert, Thierry
; TITLE OF INVENTION: COMPOUND SCREENING METHODS
; FILE REFERENCE: D00590/70008 (JRV/RE)
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US/09/549,872B
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: US 60/129,596
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: GB 9912736.7
; PRIOR FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 159
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:HUMANIZED PIG
; US-09-549-872B-13

Alignment Scores:
Pred. No.: 4,89e-12 Length: 159
Score: 150.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-724-532-1 (1-30) x US-09-549-872B-13 (1-159)
Qy 1 GlnAlaArgGlnAsnLeuGlnAsnLeuPheIleAsnPheCysLeuIleLeuIleCysLeu 20
Db 67 CAAGCAGCTCAAAAGCTTCAGAACTATTATCAATTTCTGTCTCATCTTAATATGCTTC 126
Qy 21 LeuLeuIleCysIleIleValMetLeu 30
Db 127 TTGCTGATTGTCATCATCGTATGCTTCTC 156

RESULT 3
US-09-513-999C-10799
; Sequence 10799, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Malne Edwards, J.B.
; APPLICANT: Duclet, A.
; APPLICANT: Giorlando, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59, US2, REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 10799
```

```
/ LENGTH: 480
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-10799

Alignment Scores:
Pred. No.: 1.07e-10 Length: 480
Score: 144.00 Matches: 29
Percent Similarity: 96.67% Conservative: 0
Best Local Similarity: 96.67% Mismatches: 1
Query Match: 96.00% Indels: 0
DB: 4 Gaps: 0

US-10-724-532-1 (1-30) x US-09-513-999C-10799 (1-480)
Qy 1 GlnAlaArgGlnAsnLeuGlnAsnLeuPheIleAsnPheCysLeuIleLeuIleCysLeu 20
Db 262 CAAGCAGCTCAAAAGCTTCAGAACTATTATCAATTTCTGTCTCATCTTAATATGCTTC 321
Qy 21 LeuLeuIleCysIleIleValMetLeu 30
Db 322 TTGCTGATTGTCATCATCGTATGCTTCTC 351

RESULT 4
US-09-949-016-1439
; Sequence 1439, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1439
; LENGTH: 1635
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1439

Alignment Scores:
Pred. No.: 4.3e-10 Length: 1635
Score: 144.00 Matches: 29
Percent Similarity: 96.67% Conservative: 0
Best Local Similarity: 96.67% Mismatches: 1
Query Match: 96.00% Indels: 0
DB: 4 Gaps: 0

US-10-724-532-1 (1-30) x US-09-949-016-1439 (1-1635)
Qy 1 GlnAlaArgGlnAsnLeuGlnAsnLeuPheIleAsnPheCysLeuIleLeuIleCysLeu 20
Db 248 CAAGCAGCTCAAAAGCTTCAGAACTATTATCAATTTCTGTCTCATCTTAATATGCTTC 307
Qy 21 LeuLeuIleCysIleIleValMetLeu 30
Db 308 TTGCTGATTGTCATCATCGTATGCTTCTC 337

RESULT 5
US-09-949-016-13181
; Sequence 13181, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
```

```
Db      |TGATCATCGTGTGCTTC|180  
RESULT 7  
US-09-949-016-15638  
Sequence 15638, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VERTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE; METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
PRIORITY FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 15638  
LENGTH: 69764  
TYPE: DNA  
ORGANISM: Human  
FEATURE:  
NAME/KEY: misc_feature  
LOCATION: (1)...(69764)  
OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-15638  
  
Alignment Scores:  
Pred. No.: 135  
Length: 69764  
Score: 71.00 Matches: 13  
Percent Similarity: 64.29% Conserves: 5  
Best Local Similarity: 46.43% Mismatches: 10  
Query Match: 47.33% Indels: 0  
DB: 4 Gaps: 0  
US-10-724-532-1 (1-30) x US-09-949-016-15638 (1-69764)  
QY          2 AlaArgGlAnSerLeuGlnAsnIeuheleAanPhcCysLeuIlleuCylaeUen 21  
|||...|||||:::...  
Dd    61158 GCAGGGCAAAAGSTTTCAAATAATTATGCACAACATTTTTTATTGTTATGCTGATTTC 61217  
        |||...|||  
Oy     22 leuileCyseilieleValMetreu 29  
|||...|||  
Dd    61218 TTGTGTGTTTTTATTACTTTTA 61241
```

```
RESULT 8  
US-09-270-767-10524/C  
Sequence 10524, Application US/09270767  
Patent No. 6703491  
GENERAL INFORMATION:  
APPLICANT: Homburger et al.  
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
FILE REFERENCE: File Reference: 7326-094  
CURRENT APPLICATION NUMBER: US/09/270,767  
PRIORITY FILING DATE: 1999-03-17  
NUMBER OF SEQ ID NOS: 62517  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 10524  
LENGTH: 490  
TYPE: DNA  
ORGANISM: Drosophila melanogaster  
US-09-270-767-10524  
  
Alignment Scores:  
Pred. No.: 1.19  
Length: 490  
Score: 68.00 Matches: 15  
Percent Similarity: 73.91% Conservative: 2  
Best Local Similarity: 65.22% Mismatches: 4
```

Query Match: 45.33% Indels: 2
DB: 4 Gaps: 1
US-10-724-532-1 (1-30) x US-09-270-767-10524 (1-490)
Qy 10 PheileanPheCysLeu-----lleuileCysLeuLeuileCysilleleVal 27
Db 334 TTTATTAATTTTATTTATGTTATCTTATTTGTTGTTTGTGTTGTTGTTGTT 275
Qy 28 MetleuLeu 30
Db 274 TGCCTGTTG 266
RESULT 9
US-09-270-767-11139
; Sequence 11139, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11139
; LENGTH: 553
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-11139
Alignment Scores:
Pred. No.: 1.37 Length: 553
Score: 68.00 Matches: 15
Percent Similarity: 73.91% Conservative: 2
Best Local Similarity: 65.22% Mismatches: 4
Query Match: 45.33% Indels: 2
DB: 4 Gaps: 1
US-10-724-532-1 (1-30) x US-09-270-767-11139 (1-553)
Qy 10 PheileanPheCysLeu-----lleuileCysLeuLeuileCysilleleVal 27
Db 90 TTTATTAATTTTATTTATGTTATCTTATTTGTTGTTTGTGTTGTTGTTGTT 149
Qy 28 MetleuLeu 30
Db 150 TGCCTGTTG 158
RESULT 10
US-09-270-767-14599
; Sequence 14599, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14599
; LENGTH: 992
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-14599
Alignment Scores:
Pred. No.: 2.66 Length: 992
Score: 68.00 Matches: 15
Percent Similarity: 73.91% Conservative: 2
Best Local Similarity: 65.22% Mismatches: 4
Query Match: 45.33% Indels: 2

DB: 4 Gaps: 1
US-10-724-532-1 (1-30) x US-09-270-767-14599 (1-992)
Qy 10 PheileanPheCysLeu-----lleuileCysLeuLeuileCysilleleVal 27
Db 516 TTTATTAATTTTATTTATGTTATCTTATTTGTTGTTTGTGTTGTTGTTGTT 575
Qy 28 MetleuLeu 30
Db 576 TGCCTGTTG 584
RESULT 11
US-09-949-016-12461
; Sequence 12461, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12461
; LENGTH: 93920
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12461
Alignment Scores:
Pred. No.: 866 Length: 93920
Score: 66.00 Matches: 8
Percent Similarity: 76.00% Conservative: 11
Best Local Similarity: 32.00% Mismatches: 6
Query Match: 44.00% Indels: 0
DB: 4 Gaps: 0
US-10-724-532-1 (1-30) x US-09-949-016-12461 (1-93920)
Qy 6 leuGlnanleuPheileanPheCysLeuileCysLeuLeuileCysille 25
Db 68118 TTTAATTAATGATGATATATTTTATGCTTATTAATAATGATTAATTTCTATGCTTA 68177
Qy 26 lleValMetleuLeu 30
Db 68178 TTAATGTTATTAATA 68192
RESULT 12
US-09-949-016-16853
; Sequence 16853, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012

```

; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 16853
; LENGTH: 93920
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16853

Alignment Scores:
Pred. No.:      866          Length:      93920
Score:         66.00        Matches:       8
Percent Similarity: 76.00%   Conservative: 11
Best Local Similarity: 32.00% Mismatches:    6
Query Match:     44.00%     Indels:         0
DB:              4         Gaps:           0

US-10-724-532-1 (1-30) x US-09-949-016-16853 (1-93920)

Oy      6 LeuglAenleuPheilleanPhCySleuilelleuIeCysleuLeuIleCysleu
Db      68118 TTAAATTAATGATTATATTTTATTCCTTATTAATAATATGAATAAATTTCTATGCTTA 68177

Oy      26 lleValMetleuLeu 30
Db      68178 TTATGTATTATAATA 68192

RESULT 13
US-09-949-016-136216/c
; Sequence 136216, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 136216
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-136216

Alignment Scores:
Pred. No.:      5.08          Length:      601
Score:         64.00        Matches:      14
Percent Similarity: 69.57%   Conservative: 2
Best Local Similarity: 60.87% Mismatches:    7
Query Match:     42.67%     Indels:         0
DB:              4         Gaps:           0

US-10-724-532-1 (1-30) x US-09-949-016-136216 (1-601)

Oy      5 AenleuGlAenleuPheilleanPhCySleuilelleuIeCysleuLeuIleCys 24
Db      72 AATCGCAAGACTTATCATCTTTGTTTGCTTAACAAAGTATTTGGCTCATTTTA 13

Oy      25 llelleVal 27
Db      12 ATATTGTG 4

RESULT 14
US-09-949-016-15563
; Sequence 15563, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
```

```

; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1563
; LENGTH: 58356
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15563

Alignment Scores:
Pred. NO.:          926          Length:          58356
Score:              64.00        Matches:          14
Percent Similarity: 69.57%      Conservative:    2
Best Local Similarity: 60.87%    Mismatches:     7
Query Match:        42.67%      Indels:         0
DB:                 4          Gaps:              0

US-10-724-532-1 (1-30) x US-09-949-016-15563 (1-58356)

CY      5  AaLcGtGnAneupheilleaenpCysleuIlleuIleCysleuIleuIleCys 24
          |||||
Db      38014 AACTGCGAGCACTTAATCATCTTGTGTTGCTTAACAAATGATTTTGCTCATTTTA 38073
          |||||

CY      25  IllelleVal 27
          |||||
Db      38074 ATATTGTG 38082

RESULT 15
US-09-734-674-3/C
; Sequence 3, Application US/09734674
; Patent No. 6498022
; GENERAL INFORMATION:
; APPLICANT: MET, Ming-Hui et al
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; FILE REFERENCE: CL001018
; CURRENT APPLICATION NUMBER: US/09/734,674
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 202001
; TYPE: DNA
; ORGANISM: Human
; FEATURES:
; NAME/KEY: misc_feature
; LOCATION: (1) .. (202001)
; OTHER INFORMATION: n = A,T,C or G
US-09-734-674-3

Alignment Scores:
Pred. NO.:          5.15e+03      Length:          202001
Score:              63.00        Matches:          10
Percent Similarity: 76.19%      Conservative:    6
Best Local Similarity: 47.62%    Mismatches:     5
Query Match:        42.00%      Indels:         0
DB:                 4          Gaps:              0

US-10-724-532-1 (1-30) x US-09-734-674-3 (1-202001)

CY      7  GlnbAnleupheilleaenpCysleuIleuIleuIleCysleuIleuIleCysalle 26

```

```
Db      92236  CAAATTCATTCTGCTTTTGTATATTGTTTACTAAATATANGTTGCTTCTG 92177
Qy      27    Val 27
Db      92176  GTC 92174
```

Search completed: July 7, 2005, 19:36:16
Job time : 550 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: July 7, 2005, 18:51:35 ; Search time 415 Seconds
(without alignments)
453.854 Million cell updates/sec

Title: US-10-724-532-1

Perfect score: 150

Sequence: 1 OARQNLQNLFINFCILICLLICITVML 30

Scoring table:

BLOSUM62	
Xgapop 10.0 , Xgapext 0.5	
Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 6330943 seqs, 3139157217 residues

Total number of hits satisfying chosen parameters: 12661886

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODL=frame_plus_p2n.model -DEV=xlh
-O=/cg2_1/USPFO/US1074533/runat_07072005_100331_20083/app_query.fasta_1.199
-DB=Published Applications NA -QFW=faetcap -SUFFIX=p2n.tmpb -MINMATCH=0.1
-LOOCL=0 -LOOEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCLALIGN=200 -THR SCORE=pcp -THR MAX=100
-THR MIN=0 -ALIGN=15 -MOD=LOCAL -OUTFMT=pcp -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US1074533.@CGN_1.1.741@runat_07072005_100331_20083
-NCPU=6 -ICPU=3 -NO_MMAPP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSBLOCL=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA:
1: /cg2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:
2: /cg2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:
3: /cg2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:
4: /cg2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:
5: /cg2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:
6: /cg2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:
7: /cg2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:
8: /cg2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:
9: /cg2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:
10: /cg2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:
11: /cg2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:
12: /cg2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:
13: /cg2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:
14: /cg2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:
15: /cg2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:
16: /cg2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:
17: /cg2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:
18: /cg2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:
19: /cg2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq:
20: /cg2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq:
21: /cg2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq:
22: /cg2_6/ptodata/1/pubpna/US10J_NEW_PUB.seq:
23: /cg2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:
24: /cg2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:
25: /cg2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:
26: /cg2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	150	100.0	159	15	US-10-371-101-9
2	150	100.0	159	15	US-10-371-101-9
3	144	96.0	159	19	US-10-691-412-1
4	144	96.0	159	19	US-10-691-412-1
5	144	96.0	1635	10	US-09-918-995-045
6	144	96.0	1635	10	US-09-873-367C-162
7	140	93.3	394	21	US-10-843-612A-162
8	140	93.3	394	10	US-09-918-995-4217
9	139	92.7	380	10	US-09-918-995-5377
10	139	92.7	380	10	US-09-918-995-3950
11	137	91.3	418	10	US-09-918-995-5235
12	137	91.3	108	20	US-10-724-532-3
13	137	91.3	135	20	US-10-724-532-4
14	137	91.3	135	20	US-10-724-532-5
15	130	86.7	315	20	US-10-815-514-26
16	130	86.7	315	20	US-10-815-514-26
17	130	86.7	315	21	US-10-877-930-26
18	117	78.0	492	10	US-09-918-995-17377
19	116	77.3	407	10	US-09-918-995-17377
20	68	45.3	256525	13	US-10-087-192-451
21	65	43.3	614	20	US-10-357-930-53889
22	65	43.3	43329	13	US-10-087-192-517
23	65	43.3	120581	17	US-10-085-117-247
24	64	42.7	96599	11	US-09-997-722-199
25	63.5	42.3	3673778	16	US-10-312-841-1
26	63	42.0	1368	18	US-10-424-599-50064
27	63	42.0	1680	20	US-10-729-930-303
28	63	42.0	202001	9	US-09-734-674-3
29	63	42.0	202001	14	US-10-274-990-3
30	63	42.0	202001	24	US-11-061-825-3
31	63	42.0	240102	19	US-10-367-094-192
32	62.5	41.7	397658	9	US-09-813-320-3
33	62.5	41.7	397658	24	US-11-044-879-3
34	62	41.3	409	19	US-10-674-124A-5642
35	62	41.3	457	19	US-10-674-124A-5642
36	62	41.3	34769	18	US-10-221-714A-501
37	62	41.3	62169	19	US-10-332-696-157
38	62	41.3	202251	13	US-10-087-192-985
39	62	41.3	202251	13	US-10-087-192-985
40	61.5	41.0	46675	13	US-10-087-192-985
41	61	40.7	364	19	US-10-674-124A-4970
42	61	40.7	605	13	US-10-027-632-6326
43	61	40.7	605	17	US-10-027-632-6326
44	61	40.7	623	13	US-10-027-632-280309
45	61	40.7	623	17	US-10-027-632-280309

ALIGNMENTS

RESULT 1
US-10-371-101-9
; Sequence 9, Application US/10371101
; Publication No. US2003014995A1
GENERAL INFORMATION:
APPLICANT: Zwaal, Richard
APPLICANT: Groenen, Jose
TITLE OF INVENTION: COMPOUND SCREENING METHODS
FILE REFERENCE: D00590.70035. US
CURRENT APPLICATION NUMBER: US/10/371,101
CURRENT FILING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: GB 9906670.4
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: US 60/129,596
PRIOR FILING DATE: 1999-04-15

Pred. No. is the number of results predicted by chance to have a

```
; PRIOR APPLICATION NUMBER: GB 9912736.7
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: 09/549,872
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 159
; TYPE: DNA
; ORGANISM: Sus sp.
US-10-371-101-9

Alignment Scores:
Pred. No.:      8.98e-11      Length:      159
Score:          150.00        Matches:      30
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    100.00%      Indels:      0
DB:             15           Gaps:       0

US-10-724-532-1 (1-30) x US-10-371-101-9 (1-159)

Qy      1 GlnAlaArgGlnAsnLeuGlnAsnLeuPheIleAsnPheCysLeuIleLeuIleCysLeu 20
Db      67 CACGACGCTCAAAACCTTCAGAACCTTATTCATTTCGTGTCATCTTAATATGCCTC 126

Qy      21 LeuLeuIleCysIleIleValMetLeuLeu 30
Db      127 TTGCTGATTTGTCATCATCGTATGCTTCTC 156

RESULT 2
US-10-371-101-13
; Sequence 13, Application US/10371101
; Publication No. US20030149995A1
; GENERAL INFORMATION:
; APPLICANT: Zwaal, Richard
; APPLICANT: Groenen, Jose
; APPLICANT: Bogaert, Thierry
; TITLE OF INVENTION: COMPOUND SCREENING METHODS
; FILE REFERENCE: D00590.70035 US
; CURRENT APPLICATION NUMBER: US/10/371,101
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: GB 9908670.4
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: US 60/129,596
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: GB 9912736.7
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: 09/549,872
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 159
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HUMANIZED PIG
US-10-371-101-13

Alignment Scores:
Pred. No.:      8.98e-11      Length:      159
Score:          150.00        Matches:      30
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    100.00%      Indels:      0
DB:             15           Gaps:       0

US-10-724-532-1 (1-30) x US-10-371-101-13 (1-159)

Qy      1 GlnAlaArgGlnAsnLeuGlnAsnLeuPheIleAsnPheCysLeuIleLeuIleCysLeu 20
Db      67 CACGACGCTCAAAACCTTCAGAACCTTATTCATTTCGTGTCATCTTAATATGCCTC 126

Qy      21 LeuLeuIleCysIleIleValMetLeuLeu 30
Db      127 TTGCTGATTTGTCATCATCGTATGCTTCTC 156
```

```
Db      67 CACGACGCTCAAAACCTTCAGAACCTTATTCATTTCGTGTCATCTTAATATGCCTC 126

Qy      21 LeuLeuIleCysIleIleValMetLeuLeu 30
Db      127 TTGCTGATTTGTCATCATCGTATGCTTCTC 156

RESULT 3
US-10-691-412-1
; Sequence 1, Application US/10691412
; Publication No. US20040191802A1
; GENERAL INFORMATION:
; APPLICANT: Kranaas, Evangelia G.
; APPLICANT: Kodra, Haghighi
; TITLE OF INVENTION: Phospholamban Polymorphisms and Methods of Assessment
; FILE REFERENCE: 10738-47
; CURRENT APPLICATION NUMBER: US/10/691,412
; CURRENT FILING DATE: 2003-10-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 159
; TYPE: DNA
; ORGANISM: Human
US-10-691-412-1

Alignment Scores:
Pred. No.:      5.35e-10      Length:      159
Score:          144.00        Matches:      29
Percent Similarity: 96.67%    Conservative: 0
Best Local Similarity: 96.67% Mismatches: 1
Query Match:    96.00%      Indels:      0
DB:             19           Gaps:       0

US-10-724-532-1 (1-30) x US-10-691-412-1 (1-159)

Qy      1 GlnAlaArgGlnAsnLeuGlnAsnLeuPheIleAsnPheCysLeuIleLeuIleCysLeu 20
Db      67 CACGACGCTCAAAAGCTACAGAAATCTTATTCATTTCGTGTCATCTTAATATGCCTC 126

Qy      21 LeuLeuIleCysIleIleValMetLeuLeu 30
Db      127 TTGCTGATCTGTATCATCGTATGCTTCTC 156

RESULT 4
US-09-918-995-4045
; Sequence 4045, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4045
; LENGTH: 525
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(525)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-4045

Alignment Scores:
Pred. No.:      2.39e-09      Length:      525
Score:          144.00        Matches:      29
Percent Similarity: 96.67%    Conservative: 0
Best Local Similarity: 96.67% Mismatches: 1
```



```
Query Match: 96.00% Indels: 0
DB: 10 Gaps: 0
US-10-724-532-1 (1-30) x US-09-918-995-4045 (1-525)

QY 1 GlnAATGAGlnAAsnLeuGlnAAsnLeuPheIleAAsnPhcCysLeuIleLeuIleCysLeu 20
    |||||
DB 376 CAAGCAGCTCAAAAGCTACAGATCTATTATCAATTCTGCTCATCTTAATATGCTTC 435

QY 21 LeuLeuIleCysIleIleValMetLeuLeu 30
    |||||
DB 436 TTGCTGATCTGTATCATCTGATGCTTC 465

RESULT 5
US-09-873-367C-162
; Sequence 162, Application US/09873367C
; Publication No. US20030165839A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; APPLICANT: Soppet, Daniel
; APPLICANT: Endress, Gregory
; APPLICANT: Augustus, Meena
; APPLICANT: Ebner, Reinhard
; APPLICANT: Carter, Kenneth
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
; FILE REFERENCE: 689290-64
; CURRENT APPLICATION NUMBER: US/09/873,367C
; CURRENT FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: U.S. 60/236,891
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: U.S. 60/236,842
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: U.S. 60/244,867
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: U.S. 60/245,084
; PRIOR FILING DATE: 2000-11-01
; NUMBER OF SEQ ID NOS: 1067
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 162
; LENGTH: 1635
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-873-367C-162

Alignment Scores:
Pred. No.: 9,936-09 Length: 1635
Score: 144.00 Matches: 29
Percent Similarity: 96.67% Conservative: 0
Best Local Similarity: 96.67% Mismatches: 1
Query Match: 96.00% Indels: 0
DB: 10 Gaps: 0

US-10-724-532-1 (1-30) x US-09-873-367C-162 (1-1635)

QY 1 GlnAATGAGlnAAsnLeuGlnAAsnLeuPheIleAAsnPhcCysLeuIleLeuIleCysLeu 20
    |||||
DB 248 CAAGCAGCTCAAAAGCTACAGATCTATTATCAATTCTGCTCATCTTAATATGCTTC 307

QY 21 LeuLeuIleCysIleIleValMetLeuLeu 30
    |||||
DB 308 TTGCTGATCTGTATCATCTGATGCTTC 337

RESULT 6
US-10-843-641A-162
; Sequence 162, Application US/10843641A
; Publication No. US20050064454A1
; GENERAL INFORMATION:
; APPLICANT: Avalon Pharmaceuticals, Inc.
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
; FILE REFERENCE: 689290-189
; CURRENT APPLICATION NUMBER: US/10/843,641A
```

```
; CURRENT FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: US/09/873,367
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US/09/954,531
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/09/954,456
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,436
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,832
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/964,824
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/09/967,768
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US/09/968,007
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,347
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,708
; PRIOR FILING DATE: 2001-10-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 8447
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 162
; LENGTH: 1635
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-843-641A-162

Alignment Scores:
Pred. No.: 9,936-09 Length: 1635
Score: 144.00 Matches: 29
Percent Similarity: 96.67% Conservative: 0
Best Local Similarity: 96.67% Mismatches: 1
Query Match: 96.00% Indels: 0
DB: 21 Gaps: 0

US-10-724-532-1 (1-30) x US-10-843-641A-162 (1-1635)

QY 1 GlnAATGAGlnAAsnLeuGlnAAsnLeuPheIleAAsnPhcCysLeuIleLeuIleCysLeu 20
    |||||
DB 248 CAAGCAGCTCAAAAGCTACAGATCTATTATCAATTCTGCTCATCTTAATATGCTTC 307

QY 21 LeuLeuIleCysIleIleValMetLeuLeu 30
    |||||
DB 308 TTGCTGATCTGTATCATCTGATGCTTC 337

RESULT 7
US-09-918-995-4217
; Sequence 4217, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4217
; LENGTH: 394
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: misc_feature
; LOCATION: (1)...(394)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-4217
```

Alignment Scores:
Pred. No.: 5.48e-09 Length: 394
Score: 140.00 Matches: 28
Percent Similarity: 93.33% Conservative: 0
Best Local Similarity: 93.33% Mismatches: 2
Query Match: 93.33% Indels: 0
DB: 10 Gaps: 0

US-10-724-532-1 (1-30) x US-09-918-995-4217 (1-394)

Qy 1 GlnAaagGlnAsnLeuGlnAsnLeuPheIleAsnPhcCysLeuIleLeuIleCysLeu 20
Db 248 CAAGACGCTCAAAAGCTACAGAAATCTATTATCAATTTCTGTCATCTTAATATGCTC 307

Qy 21 LeuLeuIleCysIleIleValMetLeu 30
Db 308 TTGCTGATCTGTATCATCGCGATGCTTCTC 337

RESULT 8

US-09-918-995-5377
Sequence 5377, Application US/09918995
Publication No. US20030073623A1

GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.

TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
FILE REFERENCE: 20411-756

CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20

NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 5377

LENGTH: 487

TYPE: DNA
ORGANISM: Homo sapiens

FEATURE:
NAME/KEY: misc feature

LOCATION: (1)_(487)
OTHER INFORMATION: n = A,T,C or G

US-09-918-995-5377

Alignment Scores:
Pred. No.: 7.15e-09 Length: 487
Score: 140.00 Matches: 28
Percent Similarity: 93.33% Conservative: 0
Best Local Similarity: 93.33% Mismatches: 2
Query Match: 93.33% Indels: 0
DB: 10 Gaps: 0

US-10-724-532-1 (1-30) x US-09-918-995-5377 (1-487)

Qy 1 GlnAaagGlnAsnLeuGlnAsnLeuPheIleAsnPhcCysLeuIleLeuIleCysLeu 20
Db 318 CAAGACGCTCAAAAGCTACAGAAATCTATTATCAATTTCTGTCATCTTAATATGCTC 377

Qy 21 LeuLeuIleCysIleIleValMetLeu 30
Db 378 TTGCTGATCTGTATCATCGCGATGCTTCTC 407

RESULT 9

US-09-918-995-3950
Sequence 3950, Application US/09918995
Publication No. US20030073623A1

GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.

TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
FILE REFERENCE: 20411-756

CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: US/09/235,076

PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 3950

LENGTH: 380
TYPE: DNA

ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature

LOCATION: (1)_(380)
OTHER INFORMATION: n = A,T,C or G

US-09-918-995-3950

Alignment Scores:

Pred. No.: 7.05e-09 Length: 380
Score: 139.00 Matches: 28
Percent Similarity: 93.33% Conservative: 0
Best Local Similarity: 93.33% Mismatches: 2
Query Match: 92.67% Indels: 0
DB: 10 Gaps: 0

US-10-724-532-1 (1-30) x US-09-918-995-3950 (1-380)

Qy 1 GlnAaagGlnAsnLeuGlnAsnLeuPheIleAsnPhcCysLeuIleLeuIleCysLeu 20
Db 248 CAAGACGCTCAAAAGCTACAGAAATCTATTATCAATTTCTGTCATCTTAATATGCTC 307

Qy 21 LeuLeuIleCysIleIleValMetLeu 30
Db 308 TTGCTGATCTGTATCATCGCGATGCTTCTC 337

RESULT 10

US-09-918-995-5235
Sequence 5235, Application US/09918995
Publication No. US20030073623A1

GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.

TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
FILE REFERENCE: 20411-756

CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20

NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 5235

LENGTH: 418

TYPE: DNA
ORGANISM: Homo sapiens

FEATURE:
NAME/KEY: misc feature

LOCATION: (1)_(418)
OTHER INFORMATION: n = A,T,C or G

US-09-918-995-5235

Alignment Scores:

Pred. No.: 7.95e-09 Length: 418
Score: 139.00 Matches: 28
Percent Similarity: 93.33% Conservative: 0
Best Local Similarity: 93.33% Mismatches: 2
Query Match: 92.67% Indels: 0
DB: 10 Gaps: 0

US-10-724-532-1 (1-30) x US-09-918-995-5235 (1-418)

Qy 1 GlnAaagGlnAsnLeuGlnAsnLeuPheIleAsnPhcCysLeuIleLeuIleCysLeu 20
Db 222 CAAGACGCTCAAAAGCTACAGAAATCTATTATCAATTTCTGTCATCTTAATATGCTC 281

Qy 21 LeuLeuIleCysIleIleValMetLeu 30
Db 282 TTGCTGATCTGTATCATCGCGATGCTTCTC 311

```
RESULT 11
US-10-724-532-3
; Sequence 3, Application US/10724532
; Publication No. US20040203027A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Thomas D
; TITLE OF INVENTION: Signal for Targeting Molecules to the Sarco(endo)plasmic
; FILE REFERENCE: SR RPA
; CURRENT APPLICATION NUMBER: US/10/724,532
; PRIOR FILING DATE: 2003-11-29
; PRIOR APPLICATION NUMBER: US 60/430322
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 108
; TYPE: DNA
; ORGANISM: mus musculus
US-10-724-532-3

Alignment Scores:
Pred. No.: 2,64e-09 Length: 108
Score: 137.00 Matches: 28
Percent Similarity: 93.33% Conservative: 0
Best Local Similarity: 93.33% Mismatches: 2
Query Match: 91.33% Indels: 0
DB: 20 Gaps: 0

US-10-724-532-1 (1-30) x US-10-724-532-3 (1-108)
QY 1 GlnAaTgGlnAsnLeuGlnAsnLeuPheIleAsnPhcCysLeuIleLeuIleCysLeu 20
DB 19 CAGGCCAGGACCACTCCAGAAATGCTTCATGCTTTTGTCTATTCATCTGCGCTC 78
QY 21 LeuLeuIleCysIleIleValMetLeuLeu 30
DB 79 CTGCTGATTGCAATATCGTCATGCTCGCTG 108

RESULT 12
US-10-724-532-4/c
; Sequence 4, Application US/10724532
; Publication No. US20040203027A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Thomas D
; TITLE OF INVENTION: Signal for Targeting Molecules to the Sarco(endo)plasmic
; FILE REFERENCE: SR RPA
; CURRENT APPLICATION NUMBER: US/10/724,532
; PRIOR FILING DATE: 2003-11-29
; PRIOR APPLICATION NUMBER: US 60/430322
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 108
; TYPE: DNA
; ORGANISM: mus musculus
US-10-724-532-4

Alignment Scores:
Pred. No.: 2,64e-09 Length: 108
Score: 137.00 Matches: 28
Percent Similarity: 93.33% Conservative: 0
Best Local Similarity: 93.33% Mismatches: 2
Query Match: 91.33% Indels: 0
DB: 20 Gaps: 0

US-10-724-532-1 (1-30) x US-10-724-532-4 (1-108)
QY 1 GlnAaTgGlnAsnLeuGlnAsnLeuPheIleAsnPhcCysLeuIleLeuIleCysLeu 20
DB 19 CAGGCCAGGACCACTCCAGAAATGCTTCATGCTTTTGTCTATTCATCTGCGCTC 78
QY 21 LeuLeuIleCysIleIleValMetLeuLeu 30
DB 79 CTGCTGATTGCAATATCGTCATGCTCGCTG 108

RESULT 13
US-10-724-532-5
; Sequence 5, Application US/10724532
; Publication No. US20040203027A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Thomas D
; TITLE OF INVENTION: Signal for Targeting Molecules to the Sarco(endo)plasmic
; FILE REFERENCE: SR RPA
; CURRENT APPLICATION NUMBER: US/10/724,532
; PRIOR FILING DATE: 2003-11-29
; PRIOR APPLICATION NUMBER: US 60/430322
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 135
; TYPE: DNA
; ORGANISM: mus musculus
US-10-724-532-5

Alignment Scores:
Pred. No.: 3,49e-09 Length: 135
Score: 137.00 Matches: 28
Percent Similarity: 93.33% Conservative: 0
Best Local Similarity: 93.33% Mismatches: 2
Query Match: 91.33% Indels: 0
DB: 20 Gaps: 0

US-10-724-532-1 (1-30) x US-10-724-532-5 (1-135)
QY 1 GlnAaTgGlnAsnLeuGlnAsnLeuPheIleAsnPhcCysLeuIleLeuIleCysLeu 20
DB 31 CAGGCCAGGACCACTCCAGAAATGCTTCATGCTTTTGTCTATTCATCTGCGCTC 90
QY 21 LeuLeuIleCysIleIleValMetLeuLeu 30
DB 91 CTGCTGATTGCAATATCGTCATGCTCGCTG 120

RESULT 14
US-10-724-532-6/c
; Sequence 6, Application US/10724532
; Publication No. US20040203027A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Thomas D
; TITLE OF INVENTION: Signal for Targeting Molecules to the Sarco(endo)plasmic
; FILE REFERENCE: SR RPA
; CURRENT APPLICATION NUMBER: US/10/724,532
; PRIOR FILING DATE: 2003-11-29
; PRIOR APPLICATION NUMBER: US 60/430322
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 135
; TYPE: DNA
; ORGANISM: mus musculus
US-10-724-532-6

Alignment Scores:
Pred. No.: 3,49e-09 Length: 135
Score: 137.00 Matches: 28
Percent Similarity: 93.33% Conservative: 0
Best Local Similarity: 93.33% Mismatches: 2
Query Match: 91.33% Indels: 0
DB: 20 Gaps: 0
```

US-10-724-532-1 (1-30) x US-10-724-532-6 (1-135)

OY 1 GlnAlaArgGlnAsnLeuGlnAsnLeuPheIleAsnPheCysLeuIleLeuIleCysLeu 20
Db 105 CAGGCGAGGCGAGAACCTCCAGAAAGCTTTCATTCCTTTTGTGATTCATCTGCTC 46

OY 21 LeuLeuIleCysIleIleValMetLeuLeu 30
Db 45 CTGCTGATTTGTCATTAATCTCATGCTCCTG 16

RESULT 15
US-10-815-514-26

; Sequence 26, Application US/10815514
; Publication No. US20040204361A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee
; TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
; FILE REFERENCE: 31488
; CURRENT APPLICATION NUMBER: US/10/815,514
; CURRENT FILING DATE: 2004-03-31
; PRIOR APPLICATION NUMBER: US/09/696,872
; PRIOR FILING DATE: 2000-10-26
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 315
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chimeric human PLB-KDEL
US-10-815-514-26

Alignment Scores:

Pred. No.:	8.1e-08	Length:	315
Score:	130.00	Matches:	26
Percent Similarity:	96.30%	Conservative:	0
Best Local Similarity:	96.30%	Mismatches:	1
Query Match:	86.67%	Indels:	0
DB:	20	Gaps:	0

US-10-724-532-1 (1-30) x US-10-815-514-26 (1-315)

OY 4 GlnAsnLeuGlnAsnLeuPheIleAsnPheCysLeuIleLeuIleCysLeuLeuLeuIle 23
Db 100 CAAAAGCTACAGAAATCTATTATCAATTCCTCATCTTAATAATGTCCTTGCTGATC 159

OY 24 CysIleIleValMetLeuLeu 30
Db 160 TGTATCATGCTGATGCTCTC 180

Search completed: July 7, 2005, 20:34:06
Job time : 424 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 7, 2005, 09:02:25 ; Search time 999.333 Seconds

(without alignments)
5236.654 Million cell updates/sec

Title: US-10-724-532-3

Perfect score: 108
Sequence: 1 atgcacgagagaagcctca.....gcattatcgcacgtcctcg 108

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pal:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_scs:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	52.4	48.5	858	4	RABPHLAM2
2	52.4	48.5	2841	4	OCBPPLAM
3	50.8	47.0	159	6	BD247907
4	50.8	47.0	159	6	BD247911
5	50.8	47.0	159	6	AR302003
6	50.8	47.0	159	6	AR302007
7	50.8	47.0	159	6	AX040487
8	50.8	47.0	159	6	AX040491
9	50.8	47.0	737	4	SSPLB
10	50.2	46.5	159	10	SS5853
11	50.2	46.5	386	10	SS5849
12	50.2	46.5	701	10	RNPPLAMB
13	50.2	46.5	1786	10	RATPHOLA02
14	50.2	46.5	223728	2	AC097906
15	50.2	46.5	231810	2	AC128365
16	47.6	44.1	130240	5	BX276081
17	47	43.5	648	10	BC061097
18	47	43.5	940	10	S46792
19	47	43.5	79895	2	AC100317

20	47	43.5	177018	2	AC099716	AC099716 Mus muscu
21	46.8	43.3	133901	5	BX537355	BX537355 Zebrafish
22	46.4	43.0	3312	5	CHKPLB	M59039 Chicken car
23	46.4	43.0	3423	5	CHKPLB2	M59038 Chicken pho
24	46	42.6	306	6	CO447405	CO447405 Sequence
25	46	42.6	323	9	HMPPLAM	M60411 Human phosp
26	46	42.6	480	6	AX894936	AX894936 Sequence
27	46	42.6	480	6	BD030469	BD030469 Sequence
28	46	42.6	980	9	HSP18G2	AF177764 Homo sapi
29	46	42.6	1635	6	CO718671	CO718671 Sequence
30	46	42.6	1635	6	AX329653	AX329653 Sequence
31	46	42.6	1635	9	HMPPLAM	M63603 Human phosp
32	46	42.6	1691	9	BC005269	BC005269 Homo sapi
33	46	42.6	60797	2	AL355356	AL355356 Homo sapi
34	46	42.6	66092	2	AL136974	AL136974 Homo sapi
35	46	42.6	150290	9	HS050914	Z99496 Human DNA s
36	44.4	41.1	314	4	AY514751	AY514751 Canis fam
37	44.4	41.1	832	4	DOGPHL	M16012 Canine card
38	44.4	41.1	832	4	DOGPLBA	M35393 Dog cardiac
39	44.4	41.1	2614	4	CEPHLX	Y00399 Dog phospho
40	43.6	40.4	315	6	AR121629	AR121629 Sequence
41	36	33.3	147419	9	HS738P11	AL031736 Human DNA
42	33.2	30.7	204114	2	AC108810	AC108810 Mus muscu
43	32.8	30.4	1593	9	AK098521	AK098521 Homo sapi
44	32.8	30.4	1893	9	HSR21SPA	X98294 Homo sapien
45	32.8	30.4	2254	9	AK125620	AK125620 Homo sapi

ALIGNMENTS

RESULT 1	RABPHLAM2	858 bp	DNA	linear	MAM 27-APR-1993
LOCUS	Rabbit phospholamban gene, partial exon 2.				
DEFINITION	Rabbit phospholamban gene, partial exon 2.				
ACCESSION	M63601.1	GI:165636			
VERSION	M63601.1	GI:165636			
KEYWORDS	phospholamban.				
SEGMENT	2 of 3				
SOURCE	Oryctolagus cuniculus (rabbit)				
ORGANISM	Oryctolagus cuniculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.				
AUTHORS	Fujii J., Zarain-Herzberg, A., Willard, H. F., Tada, M. and MacLennan, D. H.				
TITLE	Structure of the rabbit phospholamban gene, cloning of the human cDNA, and assignment of the gene to human chromosome 6				
JOURNAL	J. Biol. Chem. 266 (18), 11669-11675 (1991)				
MEDLINE	91268032				
PUBMED	1828805				
COMMENT	Original source text: Rabbit DNA.				
FEATURES	Location/Qualifiers				
SOURCE	1..858				
	/organism="Oryctolagus cuniculus"				
	/mol_type="genomic DNA"				
	/db_xref="taxon:9986"				
	/release_lib="Rabbit genomic"				
mrna	join(M63600.1:855..943,428..858)				
	/product="phospholamban"				
exon	428..858				
	/product="phospholamban"				
	/number=2				
CDS	524..682				
	/function="regulatory protein of sarcoplasmic reticulum Ca-ATPase"				
	/codon_start=1				
	/product="phospholamban"				
	/protein_id="AA31445.1"				
	/db_xref="GI:165639"				
	/translation="MEKVQYLTFRAIRASTIEMPOARQNLQNLFINFCILLCILL ICIIVMLL"				
ORIGIN					

Query Match 48.5%; Score 52.4; DB 4; Length 858;
Best Local Similarity 69.6%; Pred. No. 2.2e-06;
Matches 71; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

Qy 6 TGAGAGAAAGGCTCAGGCCAGACCTCCAGAACTCTTCATTCGCTTTTGTCTCAT 65
Db 577 TGAATGCTCAACAGACGTCAGAACTCCAGAACTTATTCATTTCTGTCTCAT 636
Qy 66 TCTCATCTGCCTCCGTGATTTGATATGTCATGCTCCT 107
Db 637 CTGTATATGTCCTCGCTGATCTGCATCATGCTCATGCTTCT 678

RESULT 2
OCPLHAM 2841 bp mRNA linear MAM 24-JUL-1992
DEFINITION O_cuniculus mRNA for phospholamban.
ACCESSION Y00761 GI:1661
VERSION Y00761.1
KEYWORDS phospholamban.
SOURCE Oryctolagus cuniculus (rabbit)
ORGANISM Oryctolagus cuniculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
REFERENCE 1 (bases 1 to 2841)
AUTHORS Fujii,J., Lytton,J., Tada,M. and MacLennan,D.H.
TITLE Rabbit cardiac and slow-twitch muscle express the same
JOURNAL FEBS Lett. 227 (1), 51-55 (1988)
MEDLINE 88112222
PUBMED 2962883

FEATURES
source location/Qualifiers
1..2841
/organism="Oryctolagus cuniculus"
/mol_type="mRNA"
/db_xref="taxon:9986"
178..336
/codon_start=1
/product="phospholamban"
/protein_id="CAA68730.1"
/db_xref="GI:1662"
/db_xref="GOA:P20006"
/db_xref="UniProt/Swiss-Prote:P20006"
/translation="MEKVQYLRSAIRASTIEMQQRQNLQNLFINFCLILCLL
ICITVML"

ORIGIN
Query Match 48.5%; Score 52.4; DB 4; Length 2841;
Best Local Similarity 69.6%; Pred. No. 2.5e-06;
Matches 71; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

Qy 6 TGAGAGAAAGGCTCAGGCCAGACCTCCAGAACTCTTCATTCGCTTTTGTCTCAT 65
Db 231 TGAATGCTCAACAGACGTCAGAACTCCAGAACTTATTCATTTCTGTCTCAT 290
Qy 66 TCTCATCTGCCTCCGTGATTTGATATGTCATGCTCCT 107
Db 291 CTGTATATGTCCTCGCTGATCTGCATCATGCTCATGCTTCT 332

RESULT 3
BD247907 159 bp DNA linear PAT 17-JUL-2003
DEFINITION Method for screening compounds.
ACCESSION BD247907
VERSION BD247907.1 GI:33057677
KEYWORDS JP 2002541859-A/9.
SOURCE Sus sp.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 159)

AUTHORS Zwaal,R., Groenen,J. and Bogaert,T.
TITLE Method for screening compounds
JOURNAL Patent: JP 2002541859-A 9 10-DEC-2002;
DEVGEN NV
COMMENT OS Sus sp. (pig)
PN JP 2002541859-A/9
PD 10-DEC-2002
PF 14-APR-2000 JP 2000612503
PR 15-APR-1999 GB 9908670.4,15-APR-1999 US 60/129596 PR
01-JUN-1999 GB 9912736.7
PI RICHARD ZWAAL,JOSE GROENEN,THIERRY BOGAERT
PC C12Q1/42,C12N15/09,C12Q1/02,C12N15/00
CC Method for screening compounds
FH Key Location/Qualifiers
FT source 1..159
/organism='Sus sp. (pig)'.
FEATURES
source location/Qualifiers
1..159
/organism="Sus sp. "
/mol_type="genomic DNA"
/db_xref="taxon:9826"

ORIGIN
Query Match 47.0%; Score 50.8; DB 6; Length 159;
Best Local Similarity 68.6%; Pred. No. 6e-06;
Matches 70; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

Qy 6 TGAGAGAAAGGCTCAGGCCAGACCTCCAGAACTCTTCATTCGCTTTTGTCTCAT 65
Db 54 TGAATGCTCAACAGACGTCAGAACTCCAGAACTTATTCATTTCTGTCTCAT 113
Qy 66 TCTCATCTGCCTCCGTGATTTGATATGTCATGCTCCT 107
Db 114 CTATATATGCTCTTGCTGATTTGCATCATGCTGATGCTTCT 155

RESULT 4
BD247911 159 bp DNA linear PAT 17-JUL-2003
LOCUS BD247911
DEFINITION Method for screening compounds.
ACCESSION BD247911
VERSION BD247911.1 GI:33057681
KEYWORDS JP 2002541859-A/13.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 159)
AUTHORS Zwaal,R., Groenen,J. and Bogaert,T.
TITLE Method for screening compounds
JOURNAL Patent: JP 2002541859-A 13 10-DEC-2002;
DEVGEN NV
COMMENT OS Artificial Sequence
PN JP 2002541859-A/13
PD 10-DEC-2002
PF 14-APR-2000 JP 2000612503
PR 15-APR-1999 GB 9908670.4,15-APR-1999 US 60/129596 PR
01-JUN-1999 GB 9912736.7
PI RICHARD ZWAAL,JOSE GROENEN,THIERRY BOGAERT
PC C12Q1/42,C12N15/09,C12Q1/02,C12N15/00
CC Description of Artificial Sequence: HUMANIZED PIG PLB cDNA FH
FH Key Location/Qualifiers
FT source 1..159
/organism='Artificial Sequence'.
FEATURES
source location/Qualifiers
1..159
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 47.0%; Score 50.8; DB 6; Length 159;
Best Local Similarity 68.6%; Pred. No. 6e-06;
Matches 70; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 7, 2005, 09:02:25 ; Search time 205.111 Seconds

(without alignment)
3117.004 Million cell updates/sec

Title: US-10-724-532-3

Perfect score: 108
Sequence: 1 atcagtagagagaagcctca.....gcattatcgtcctctcg 108

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*

1: geneeqn1980a:*\n2: geneeqn1990a:*\n3: geneeqn2000a:*\n4: geneeqn2001a:*\n5: geneeqn2001b:*\n6: geneeqn2002a:*\n7: geneeqn2002b:*\n8: geneeqn2003a:*\n9: geneeqn2003b:*\n10: geneeqn2003c:*\n11: geneeqn2003d:*\n12: geneeqn2004a:*\n13: geneeqn2004b:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50.8	47.0	159	3 AAC64967	AAC64967 Pig phosp
2	50.2	46.5	701	10 ADB53082	ADB53082 Primary r
3	46.5	42.6	159	13 ADR97285	ADR97285 Human rho
4	46.4	42.6	306	6 ABR22344	ABR22344 Human ORF
5	46.4	42.6	480	3 AAC06724	AAC06724 Human sec
6	46.4	42.6	525	9 ACH16833	ACH16833 Human adu
7	46.4	42.6	1635	6 ABL61825	ABL61825 Colon ade
8	46.4	42.6	1635	12 ADN04087	ADN04087 Antispori
9	46.4	42.6	1712	12 ADP21384	ADP21384 Gene PLN
10	45.4	41.7	380	9 ACH16738	ACH16738 Human adu
11	45.4	41.7	418	9 ACH18023	ACH18023 Human adu
12	44.4	41.1	394	9 ACH17005	ACH17005 Human adu
13	44.4	41.1	487	9 ACH18165	ACH18165 Human adu
14	43.6	40.4	312	3 AAZ50498	AAZ50498 KDEL rece
15	41.2	38.1	407	9 ACH16630	ACH16630 Human adu
16	38.3	35.2	492	9 ACH30165	ACH30165 Human tes
17	36.3	33.3	147419	6 ABR83574	ABR83574 Human CDN
18	32.8	30.4	652	6 ABQ60653	ABQ60653 Human COL
19	32.8	30.4	1896	12 ADP07907	ADP07907 Human RAD
20	32.8	30.4	2419	5 ADL62294	ADL62294 Human ova

C 21	32.8	30.4	2422	10 ADC37617	ADC37617 Human nuc
C 22	32.8	30.4	3647	6 ABR83658	ABR83658 Human CDN
C 23	32.8	30.4	3647	10 ADF81412	ADF81412 Leukaemia
C 24	32.8	30.4	3647	13 ADR25399	ADR25399 Breast ca
C 25	32.8	30.4	3647	13 ACN38837	ACN38837 Tumour-as
C 26	32.8	30.4	3708	2 AAZ77530	AAZ77530 Human ova
C 27	32.8	30.4	3748	3 AAC77686	AAC77686 Human can
C 28	32.8	30.4	3925	12 ADQ21778	ADQ21778 Human bof
C 29	32.8	29.6	6481	4 AA159183	AA159183 Human pol
C 30	32.8	29.6	6481	5 ADO99406	ADO99406 DNA encod
C 31	32.8	29.6	6481	9 ADB49166	ADB49166 Novel hum
C 32	32.8	29.6	6536	3 AAC75801	AAC75801 Human ORF
C 33	32.8	29.6	10625	5 AAC85836	AAC85836 Nucleotid
C 34	32.8	29.6	10625	6 AAL41031	AAL41031 DNA encod
C 35	31.2	28.9	473	13 ADQ79072	ADQ79072 Novel can
C 36	30.4	28.1	1938	11 ACN44341	ACN44341 Mouse mRN
C 37	30.4	28.1	2175	2 AAX24906	AAX24906 Mouse eLo
C 38	30.2	28.0	639	8 ABT14895	ABT14895 Pathogen
C 39	30.2	28.0	639	8 ACF73801	ACF73801 Staphyloc
C 40	30.2	27.8	415	4 AA113308	AA113308 Probe #32
C 41	30.2	27.8	415	4 ABA55007	ABA55007 Human foe
C 42	30.2	27.8	415	4 AA134661	AA134661 Probe #33
C 43	30.2	27.8	415	4 ABA44562	ABA44562 Human bre
C 44	30.2	27.8	415	4 ABA24770	ABA24770 Probe #32
C 45	30.2	27.8	415	4 AAK28730	AAK28730 Human bon

ALIGNMENTS

RESULT 1

AAC64967 standard; CDNA, 159 BP.

ID	AAC64967	standard; CDNA, 159 BP.
XX		
AC	AAC64967;	
XX		
DT	09-FEB-2001 (first entry)	
XX		
DE	Pig phospholamban cDNA.	
XX		
KW	Pig, sarco/endoplasmic reticulum calcium ATPase; SERCA; signalling;	
KW	cardiac hypertrophy; heart failure; hypertension; Daxler-White disease;	
KW	Brody's disease; diabetes; ss.	
OS	Sus scrofa.	
XX		
PN	GB2349217-A.	
XX		
PD	25-OCT-2000.	
XX		
PF	14-APR-2000; 2000GB-00009363.	
XX		
PR	15-APR-1999; 99GB-00008670.	
PR	15-APR-1999; 99US-0129596P.	
PR	01-JUN-1999; 99GB-00012736.	
XX		
PA	(DEWG-) DEWGEN NV.	
PI	Zwaal R, Groenen J, Bogaert T;	
XX		
DR	WPI, 2000-658082/64.	
XX		
PT	Identifying modulators of sarco/endoplasmic reticulum calcium ATPase,	
PT	useful potentially for treating disorders of calcium homeostasis, e.g.	
PT	cardiac hypertrophy.	
XX		
PS	Disclosure; Fig 11; 108pp; English.	
XX		
CC	The present invention is concerned with methods of using C. elegans to	
CC	identify compounds which are capable of up- and down-regulating the	
CC	activity of the sarco/endoplasmic reticulum calcium ATPase (SERCA). This	
CC	protein is involved in cell signalling, and elevated levels affect	
CC	cellular processes such as contraction, secretion and cell cycling. The	

CC methods can be used to identify compounds for use in the treatment of
CC some muscle pathologies, cardiac hypertrophy, heart failure,
CC hypertension, diabetes, Darier-White disease and Brody's disease
XX
50 Sequence 159 BP; 45 A; 41 C; 22 G; 51 T; 0 U; 0 Other;
Query Match 47.0%; Score 50.8; DB 3; Length 159;
Best Local Similarity 68.6%; Pred. No. 3.3e-06;
Matches 70; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
OY 6 TGAGAGAGGCTCAGGCGCAGACCTCCAGAAATGCTTTCATTCCTTTTGTCTGAT 65
DB 54 TGAATGCCCCAGAGCGCTCGAACCCTTCAGAACTTATTCATTTCTGTCTCAT 113
OY 66 TCTCATCTGCTCCTCGCTGATTTGCATTTATGCTCATGCTCT 107
DB 114 CTTATATATGCTCTTCTGCTGATTTGCATTCATGCTGATCTTCT 155
RESULT 2
ID ADB53082 standard; DNA; 701 BP.
XX ADB53082;
XX
DT 04-DEC-2003 (first entry)
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3624.
XX
KM toxic effect; gene expression profile; hepatotoxicity; diagnostic marker;
KM toxicity marker; toxicity progression; drug screening;
KM primary rat hepatocyte toxicity modelling; gene; db.
XX
OS Rattus norvegicus.
XX
FN WO2003065993-A2.
XX
PD 14-AUG-2003.
XX
PE 04-FEB-2003; 2003WO-US003482.
XX
PR 04-FEB-2002; 2002US-0353171P.
PR 13-MAR-2002; 2002US-0363534P.
PR 08-APR-2002; 2002US-0370248P.
PR 10-APR-2002; 2002US-0371134P.
PR 10-APR-2002; 2002US-0371135P.
PR 10-APR-2002; 2002US-0371150P.
PR 11-APR-2002; 2002US-0371413P.
PR 19-APR-2002; 2002US-0373601P.
PR 22-APR-2002; 2002US-0374139P.
PR 08-MAY-2002; 2002US-0378370P.
PR 09-MAY-2002; 2002US-0378652P.
PR 09-MAY-2002; 2002US-0378653P.
PR 09-MAY-2002; 2002US-0378655P.
PR 09-JUL-2002; 2002US-0394230P.
PR 09-JUL-2002; 2002US-0394253P.
PR 04-SEP-2002; 2002US-0407688P.
PR 28-JAN-2003; 2003US-0442900P.
XX
PA (GENE-) GENE LOGIC INC.
XX
PI Mendrick D, Porter M, Johnson K, Higgs B, Castle A, Orr M;
PI Elashoff M;
XX
DR WPI; 2003-731472/69.
XX
PT Determining if a compound induces a toxic effect on a tissue or cell, for
PT identifying hepatotoxic compounds, comprises comparing a gene expression
PT profile of a tissue or cell sample to a database of Tox mean and non-Tox
PT mean values.
XX
PS Claim 44; SEQ ID NO 3624; 874bp; English.

XX
CC The present invention describes a method for determining whether a
CC compound induces a toxic effect on a tissue or cell. The method comprises
CC preparing a gene expression profile of a tissue or cell sample exposed to
CC the compound, and comparing the gene expression profile to a database
CC comprising data or information on the Tox mean and non-Tox mean value.
CC The method is useful for predicting or identifying at least one toxic
CC effect, particularly hepatotoxicity, of a test or unknown compound. The
CC genes listed in the specification are useful as diagnostic or toxicity
CC markers for the prediction or identification of the physiological state
CC of tissue or cell sample that has been exposed to a compound, or to
CC identify or predict the toxic effects of a compound or an agent. These
CC may also be used as markers for monitoring toxicity progression or for
CC drug screening. The present sequence represents a primary rat hepatocyte
CC toxicity modelling related gene sequence from the present invention.
XX
SQ Sequence 701 BP; 184 A; 178 C; 141 G; 198 T; 0 U; 0 Other;
Query Match 46.5%; Score 50.2; DB 10; Length 701;
Best Local Similarity 68.0%; Pred. No. 8.1e-06;
Matches 70; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
OY 6 TGAGAGAGGCTCAGGCGCAGACCTCCAGAAATGCTTTCATTCCTTTTGTCTGAT 65
DB 227 TGAATGCCCCAGAGCGCTCGAACCCTTCAGAACTTATTCATTTCTGTCTCAT 286
OY 66 TCTCATCTGCTCCTCGCTGATTTGCATTTATGCTCATGCTCTG 108
DB 287 CTTGATATGCTCTGCTGCTGATATGATCATCATGTGATGTTCTG 329
RESULT 3
ID ADR97285 standard; DNA; 159 BP.
XX ADR97285;
XX
DT 16-DEC-2004 (first entry)
DE Human phospholamban polymorphism fragment DNA.
XX
KM ds; human; phospholamban; polymorphism; cardiovascular disease.
XX
OS Homo sapiens.
XX
FN US2004191802-A1.
XX
PD 30-SEP-2004.
XX
PF 22-OCT-2003; 2003US-00691412.
XX
PR 22-OCT-2002; 2002US-0420295P.
XX
PA (KRAN/) KRANTAS B G.
PA (HAGH/) HAGHIGHI K.
XX
PI Krantias EG, Haghighi K;
XX
DR WPI; 2004-689841/67.
XX
PT Phospholamban polymorphism assessment in individual, for determining risk
PT for developing cardiovascular disease, by comparing analysis of the
PT nucleotide fragment with a predetermined phospholamban nucleotide
PT fragment sequence.
XX
PS Claim 15; SEQ ID NO 1; 15bp; English.
XX
CC The invention relates to a method of phospholamban polymorphism
CC assessment in an individual which comprises comparing the analysis of the
CC nucleotide fragment with a predetermined phospholamban nucleotide
CC fragment sequence to determine whether the individual carries a
CC phospholamban polymorphism. The methods and phospholamban polymorphism
CC fragment are useful for determining if an individual is at risk for

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 7, 2005, 09:02:25 ; Search time 1353.33 Seconds
(without alignment)
3037.641 Million cell updates/sec

Title: US-10-724-532-3
Perfect score: 108
Sequence: 1 atgcatacgagaagcgctca.....gcattatcgcatgctctcg 108

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
EST:
1: gb_est1:
2: gb_est2:
3: gb_hic:
4: gb_est3:
5: gb_est4:
6: gb_est5:
7: gb_est6:
8: gb_est1:
9: gb_est2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50.8	47.0	381	5	BX669692 BX669692
2	50.8	47.0	702	5	BX922974 BX922974
3	50.8	47.0	724	5	BX674983 BX674983
4	50.8	47.0	740	5	BX924154 BX924154
5	50.8	47.0	758	5	BX923697 BX923697
6	50.8	47.0	811	7	CK49263 CK49263
7	50.2	46.5	179	2	BE113353 BE113353
8	50.2	46.5	377	2	BF547322 BF547322
9	50.2	46.5	417	1	AI322542 AI322542
10	50.2	46.5	439	2	BE115006 BE115006
11	50.2	46.5	449	2	BE098177 BE098177
12	50.2	46.5	449	2	BE098177 BE098177
13	50.2	46.5	451	4	BI288911 BI288911
14	50.2	46.5	454	4	BE099930 BE099930
15	50.2	46.5	476	2	BF525258 BF525258
16	50.2	46.5	480	7	CR471116 CR471116
17	50.2	46.5	487	7	CG379827 CG379827
18	50.2	46.5	498	1	AI603160 AI603160
19	50.2	46.5	511	4	BF395370 BF395370
20	50.2	46.5	513	4	BI296789 BI296789
21	50.2	46.5	518	2	BE112568 BE112568
22	50.2	46.5	527	2	BF395607 BF395607
23	50.2	46.5	528	2	BF395670 BF395670
24	50.2	46.5	540	2	BF395398 BF395398

c	25	50.2	46.5	575	4	BI290034	UI-R-DKO-
	26	50.2	46.5	589	2	BF525010	BF525010
	27	50.2	46.5	508	1	AI103929	EST13218
c	28	50.2	46.5	699	7	CK358482	CK358482
	29	50.2	46.5	710	7	CK359590	CK359590
	30	50.2	46.5	718	7	CK358464	CK358464
	31	50.2	46.5	719	7	CK356296	CK356296
	32	50.2	46.5	731	7	CK357243	CK357243
	33	50.2	46.5	737	7	CK357232	CK357232
	34	50.2	46.5	738	7	CK355359	CK355359
	35	50.2	46.5	738	7	CK357123	CK357123
	36	50.2	46.5	744	7	CK356439	CK356439
	37	50.2	46.5	744	7	CK357747	CK357747
	38	50.2	46.5	745	7	CK355314	CK355314
	39	50.2	46.5	745	7	CK356371	CK356371
	40	50.2	46.5	748	7	CK359219	CK359219
	41	50.2	46.5	754	7	CK355445	CK355445
	42	50.2	46.5	758	7	CK355453	CK355453
	43	50.2	46.5	758	7	CK357746	CK357746
	44	50.2	46.5	762	7	CK359188	CK359188
	45	50.2	46.5	764	7	CK357447	CK357447

ALIGNMENTS

RESULT 1
BX669692
LOCUS BX669692 381 bp mRNA linear EST 07-MAY-2004
DEFINITION BX669692 Sus scrofa library (scac) Sus scrofa cDNA clone
ACCESSION scac00281.c.02 Sprim, mRNA sequence.
VERSION BX669692
KEYWORDS BX669692.1 GI:37979481
SOURCE EST
ORGANISM Sus scrofa (pig)
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
1 (bases 1 to 381)
REFERENCE Bonner, A., Tosser-Klopp, G., Benne, F., Cabau, C., Villiger, S.,
Soares, M., Bonaldo, F. and Hately, F.
A Pig Normalised Multi-Tissue cDNA Library
Unpublished (2003)
CONTACT: Tosser-Klopp G
Genetique Animale
Institut National de la Recherche Agronomique
Chemin de Borde-Rouge - Auzeville BP27, 31326 Castanet-Tolosan
cedex, FRANCE
Tel: 33 (0) 5.61.28.51.14
Fax: 33 (0) 5.61.28.53.08
Email: tosser@toulouse.inra.fr
Sequence cleaned of vector, adaptor and repetitions. Contact us
at sigenastupport@journ.inra.fr to obtain the chromatogram of this
sequence.
Plate: 0028 row: c column: 2.

FEATURES

source
1..381
Location/Qualifiers
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="scac00281.c.02"
/tissue_type="mixed"
/clone_lib="Sus scrofa library (scac)"
/note="Vector: pTRIP-pac vector; tissues: adipose tissue,
brain, kidney, liver, muscle, ovary, testis, heart,
hypothalamus, pancreas, skin, spleen, thymus, placenta,
pituitary gland, seminal vesicle, small intestine,
uterus, adrenals, bulbo urethral gland, cerebral trunk,
epididymis, female gonad, gall-bladder, hippocampus,
large intestine, male gonad, melanocytes, stomach, udder"

ORIGIN

Query Match

47.0%; Score 50.8; DB 5; Length 381;

Best Local Similarity 68.6%; Pred. No. 0.00012;
Matches 70; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

OY 6 TGAAGAGGCTCAGGCGACAGCAACCTCCAGAAATGCTTTCATTCGTTTTCAT 65
DB 82 TGAATGCTCAACAGACGCTCAAAACCTTCAGAACCTATTATCAATTCGTCTCAT 141
OY 66 TCTCATCTGCTCCTGCTGATTTGATTCATTCGTCATGCTCT 107
DB 142 CTTAATATGCTCTTCTGCTGATTTGATTCATTCGTCATGCTCT 183

RESULT 2
BX922974
LOCUS
DEFINITION BX922974 Sus Scrofa library (scan) Sus scrofa cDNA clone
ACCESSION BCAN0013d.f.14 5prim, mRNA sequence.
VERSION BX922974
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa

REFERENCE 1 (bases 1 to 702)
AUTHORS Bonnet,A., Tosser-Klopp,G., Benne,F., Cabau,C., Villegier,S., Soares,M., Bonaldo,F. and Hately,F.
TITLE A Pig Normalised Multi-Tissue cDNA Library
JOURNAL Unpublished (2003)
COMMENT Contact: Tosser-Klopp G
Genetique Animale
Institut National de la Recherche Agronomique
Chemin de Borde-Rouge - Auzeville BP27, 31326 Castanet-Tolosan
cedex, FRANCE
Tel: 33 (0) 5.61.28.51.14
Fax: 33 (0) 5.61.28.53.08
Email: tosser@toulouse.inra.fr
Sequence cleaned of vector, adaptor and repetitions. Contact us
at sigenastupport@jouy.inra.fr to obtain the chromatogram of this
sequence.
Plate: 0013 row: j column: 14.
Location/Qualifiers
1..702
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="scan0013d.f.14"
/tissue_type="mixed"
/dev_stage="from embryos to adults"
/note="Tissues: adipose tissue, brain, kidney, liver, muscle, ovary, testis, heart, hypothalamus, pancreas, skin, spleen, thymus, placenta, pituitary gland, seminal vesicle, small intestine, uterus, adrenals, bulbo urethral gland, cerebral trunk, epididymis, female gonad, gall-bladder, hippocampus, large intestine, male gonad, melanocytes, stomach, udder"

FEATURES
source

ORIGIN
Query Match 47.0%; Score 50.8; DB 5; Length 702;
Best Local Similarity 68.6%; Pred. No. 0.00013;
Matches 70; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

OY 6 TGAAGAGGCTCAGGCGACAGCAACCTCCAGAAATGCTTTCATTCGTTTTCAT 65
DB 216 TGAATGCTCAACAGACGCTCAAAACCTTCAGAACCTATTATCAATTCGTCTCAT 275
OY 66 TCTCATCTGCTCCTGCTGATTTGATTCATTCGTCATGCTCT 107
DB 276 CTTAATATGCTCTTCTGCTGATTTGATTCATTCGTCATGCTCT 317

RESULT 3

BX674983
LOCUS
DEFINITION BX674983 Sus Scrofa library (scan) Sus scrofa cDNA clone
ACCESSION BCAN0013d.f.23 5prim, mRNA sequence.
VERSION BX674983
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa

REFERENCE 1 (bases 1 to 724)
AUTHORS Bonnet,A., Tosser-Klopp,G., Benne,F., Cabau,C., Villegier,S., Soares,M., Bonaldo,F. and Hately,F.
TITLE A Pig Normalised Multi-Tissue cDNA Library
JOURNAL Unpublished (2003)
COMMENT Contact: Tosser-Klopp G
Genetique Animale
Institut National de la Recherche Agronomique
Chemin de Borde-Rouge - Auzeville BP27, 31326 Castanet-Tolosan
cedex, FRANCE
Tel: 33 (0) 5.61.28.51.14
Fax: 33 (0) 5.61.28.53.08
Email: tosser@toulouse.inra.fr
Sequence cleaned of vector, adaptor and repetitions. Contact us
at sigenastupport@jouy.inra.fr to obtain the chromatogram of this
sequence.
Plate: 0039 row: h column: 23.
Location/Qualifiers
1..724
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="scan0039i.h.23"
/tissue_type="mixed"
/clone_lib="Sus Scrofa library (scan)"
/note="Vector: pT73d-pac vector; tissues: adipose tissue, brain, kidney, liver, muscle, ovary, testis, heart, hypothalamus, pancreas, skin, spleen, thymus, placenta, pituitary gland, seminal vesicle, small intestine, uterus, adrenals, bulbo urethral gland, cerebral trunk, epididymis, female gonad, gall-bladder, hippocampus, large intestine, male gonad, melanocytes, stomach, udder"

FEATURES
source

ORIGIN
Query Match 47.0%; Score 50.8; DB 5; Length 724;
Best Local Similarity 68.6%; Pred. No. 0.00013;
Matches 70; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

OY 6 TGAAGAGGCTCAGGCGACAGCAACCTCCAGAAATGCTTTCATTCGTTTTCAT 65
DB 237 TGAATGCTCAACAGACGCTCAAAACCTTCAGAACCTATTATCAATTCGTCTCAT 296
OY 66 TCTCATCTGCTCCTGCTGATTTGATTCATTCGTCATGCTCT 107
DB 297 CTTAATATGCTCTTCTGCTGATTTGATTCATTCGTCATGCTCT 338

RESULT 4
BX924154
LOCUS
DEFINITION BX924154 Sus Scrofa library (scan) Sus scrofa cDNA clone
ACCESSION BCAN0013d.f.23 5prim, mRNA sequence.
VERSION BX924154
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa

REFERENCE 1 (bases 1 to 740)
AUTHORS Bonnet,A., Tosser-Klopp,G., Benne,F., Cabau,C., Villegier,S., Soares,M., Bonaldo,F. and Hately,F.
TITLE A Pig Normalised Multi-Tissue cDNA Library
JOURNAL Unpublished (2003)
COMMENT Contact: Tosser-Klopp G
Genetique Animale
Institut National de la Recherche Agronomique
Chemin de Borde-Rouge - Auzeville BP27, 31326 Castanet-Tolosan
cedex, FRANCE
Tel: 33 (0) 5.61.28.51.14
Fax: 33 (0) 5.61.28.53.08
Email: tosser@toulouse.inra.fr
Sequence cleaned of vector, adaptor and repetitions. Contact us
at sigenastupport@jouy.inra.fr to obtain the chromatogram of this
sequence.
Plate: 0039 row: h column: 23.
Location/Qualifiers
1..740
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="scan0039i.h.23"
/tissue_type="mixed"
/clone_lib="Sus Scrofa library (scan)"
/note="Vector: pT73d-pac vector; tissues: adipose tissue, brain, kidney, liver, muscle, ovary, testis, heart, hypothalamus, pancreas, skin, spleen, thymus, placenta, pituitary gland, seminal vesicle, small intestine, uterus, adrenals, bulbo urethral gland, cerebral trunk, epididymis, female gonad, gall-bladder, hippocampus, large intestine, male gonad, melanocytes, stomach, udder"

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Comugen Ltd.

OM nucleic - nucleic search, using SW model

Run on: July 7, 2005, 09:02:25 ; Search time 61.7778 Seconds
(without alignments)
2860.541 Million cell updates/sec

Title: US-10-724-532-3

Perfect score: 108
Sequence: 1 atgcatagagaagagcctca.....gcatacgcatacgtctctg 108

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*

1: /cgn2_6/prodata/1/ina/5A_COMB.seq:*\n2: /cgn2_6/prodata/1/ina/5B_COMB.seq:*\n3: /cgn2_6/prodata/1/ina/6A_COMB.seq:*\n4: /cgn2_6/prodata/1/ina/6B_COMB.seq:*\n5: /cgn2_6/prodata/1/ina/PCTUS_COMB.seq:*\n6: /cgn2_6/prodata/1/ina/backfillseq1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50.8	47.0	159	4	US-09-549-872B-9 Sequence 9, Appl
2	50.8	47.0	159	4	US-09-549-872B-13 Sequence 13, Appl
3	46	42.6	1480	4	US-09-513-999C-10799 Sequence 10799, A
4	46	42.6	1635	4	US-09-949-016-1439 Sequence 1439, Ap
5	46	42.6	16062	4	US-09-949-016-13181 Sequence 13181, A
6	43.6	40.4	315	3	US-09-124-671-26 Sequence 26, Appl
7	32	29.6	6481	4	US-09-620-312D-1076 Sequence 1076, Ap
8	30.4	28.1	2175	4	US-08-914-999-3 Sequence 3, Appl
9	30.2	28.0	74353	4	US-09-949-016-15336 Sequence 15336, A
10	29	26.9	4474	4	US-09-513-999C-1161 Sequence 1161, Ap
11	29	26.9	1123	3	US-09-188-930-28 Sequence 28, Appl
12	29	26.9	1123	3	US-09-188-930-203 Sequence 203, Appl
13	29	26.9	1123	3	US-09-312-283C-28 Sequence 28, Appl
14	29	26.9	1123	3	US-09-312-283C-203 Sequence 203, Appl
15	28.8	26.7	879	4	US-09-489-039A-5041 Sequence 5041, Ap
16	28.4	26.3	162914	4	US-09-949-016-15578 Sequence 15578, A
17	27.8	25.7	72	3	US-08-945-734-11 Sequence 11, Appl
18	27.8	25.7	72	3	US-09-558-797-11 Sequence 11, Appl
19	27.8	25.7	72	5	PCT-US96-09451-11 Sequence 11, Appl
20	27.8	25.7	568	4	US-08-956-171E-999 Sequence 999, App
21	27.8	25.7	568	4	US-08-781-986A-999 Sequence 999, App
22	27.8	25.7	1920	3	US-09-160-496C-4 Sequence 4, Appl
23	27.8	25.7	48313	4	US-09-949-016-17088 Sequence 17088, A
24	27.8	25.7	65424	4	US-09-949-016-12426 Sequence 12426, A
25	27.6	25.6	601	4	US-09-949-016-202802 Sequence 202802, A
26	27.6	25.6	26050	4	US-09-949-016-17449 Sequence 17449, A
27	27.6	25.6	98844	3	US-09-791-211-10 Sequence 10, Appl

28	27.6	25.6	143776	4	US-09-949-001-29 Sequence 29, Appl
29	27.6	25.6	144034	4	US-09-949-001-35 Sequence 35, Appl
30	27.4	25.4	483	4	US-09-583-110-2272 Sequence 2272, Ap
31	27.4	25.4	489	4	US-09-107-433-492 Sequence 492, App
32	27.4	25.4	601	4	US-09-949-016-82861 Sequence 82861, A
33	27.4	25.4	957	1	US-08-309-182B-1 Sequence 1, Appl
34	27.4	25.4	1117	4	US-09-552-225A-11 Sequence 11, Appl
35	27.4	25.4	1851	4	US-09-949-016-3036 Sequence 3036, Ap
36	27.4	25.4	2120	3	US-09-149-476-160 Sequence 160, Appl
37	27.4	25.4	2628	4	US-09-774-528-27 Sequence 27, Appl
38	27.4	25.4	8590	4	US-09-949-016-5562 Sequence 5562, Ap
39	27.4	25.4	10300	4	US-09-949-016-636 Sequence 636, App
40	27.4	25.4	38575	4	US-09-949-016-17304 Sequence 17304, A
41	27.4	25.4	119153	4	US-09-949-016-12378 Sequence 12378, A
42	27.4	25.4	213456	4	US-09-820-007-3 Sequence 3, Appl
43	27.4	25.4	323820	4	US-09-949-016-14139 Sequence 14139, A
44	27.2	25.2	7644	4	US-09-949-016-17610 Sequence 17610, A
45	27	25.0	372	4	US-09-270-767-5510 Sequence 5510, Ap

ALIGNMENTS

```
RESULT 1
US-09-549-872B-9
; Sequence 9, Application US/09549872B
; Patent No. 6540996
; GENERAL INFORMATION:
; APPLICANT: Zwaal, Richard
; APPLICANT: Groenen, Jose
; APPLICANT: Bogaert, Thierry
; TITLE OF INVENTION: COMPOUND SCREENING METHODS
; FILE REFERENCE: D00590/70008 (JRV/RE)
; CURRENT APPLICATION NUMBER: US/09/549,872B
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: GB 9908670.4
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: US 60/129,596
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: GB 9912736.7
; PRIOR FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 159
; TYPE: DNA
; ORGANISM: Sus sp.
US-09-549-872B-9
Query Match
Best Local Similarity 47.0%; Score 50.8; DB 4; Length 159;
Matches 70; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
QY 6 TGAGGAAGGCGCTCAGGCGAGACCTCCAGAACCTTCATGCTTTTGTCTGAT 65
DB 54 TGAATGCGCTCAACAGACGCTCAAACTTCAGAACCTTATTCATTTCTCTAT 113
DB 114 CTTATATGCGCTTCGTGATTCATGTCATGTCATGTCATGTCAT 155
RESULT 2
US-09-549-872B-13
; Sequence 13, Application US/09549872B
; Patent No. 6540996
; GENERAL INFORMATION:
; APPLICANT: Zwaal, Richard
; APPLICANT: Groenen, Jose
; APPLICANT: Bogaert, Thierry
; TITLE OF INVENTION: COMPOUND SCREENING METHODS
; FILE REFERENCE: D00590/70008 (JRV/RE)
; CURRENT APPLICATION NUMBER: US/09/549,872B
```

```

; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: GB 9908670.4
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: US 60/129,596
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: GB 9912736.7
; PRIOR FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 13
; LENGTH: 159
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HUMANIZED PIG
; OTHER INFORMATION: PLB cDNA
US-09-549-872B-13
```

```

Query Match          47.0%; Score 50.8; DB 4; Length 159;
Best Local Similarity 68.6%; Pred. No. 5.6e-08;
Matches 70; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
```

```

QY 6 TGAGAGAAAGGCTCAGGCGCAGGAGCAAGCTCCAGAAATGCTTTCATTTGTTCTGAT 65
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 54 TGAATGCGCTCAACAGACGCTCAAAAGCTTCAGAACTTATTCATTTCTGTCTCAT 113
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 66 TCTCATGCGCTCCTGCTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 107
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 114 CTTAATATGCTCTTCTGCTGATTTGATTTGATTTGATTTGATTTGATTTGATTTCT 155
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

RESULT 3

```

US-09-513-999C-10799
; Sequence 10799, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclerc, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59. US2, REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 10799
; LENGTH: 480
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-10799
```

```

Query Match          42.6%; Score 46; DB 4; Length 480;
Best Local Similarity 65.7%; Pred. No. 4e-06;
Matches 67; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
```

```

QY 6 TGAGAGAAAGGCTCAGGCGCAGGAGCAAGCTCCAGAAATGCTTTCATTTGTTCTGAT 65
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 249 TGAATGCGCTCAACAGACGCTCAAAAGCTTCAGAACTTATTCATTTCTGTCTCAT 308
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 66 TCTCATGCGCTCCTGCTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 107
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 309 CTTAATATGCTCTTCTGCTGATTTGATTTGATTTGATTTGATTTGATTTGATTTCT 350
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

RESULT 4

```

US-09-949-016-1439
; Sequence 1439, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
```

```

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1439
; LENGTH: 1635
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1439
```

```

Query Match          42.6%; Score 46; DB 4; Length 1635;
Best Local Similarity 65.7%; Pred. No. 6.7e-06;
Matches 67; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
```

```

QY 6 TGAGAGAAAGGCTCAGGCGCAGGAGCAAGCTCCAGAAATGCTTTCATTTGTTCTGAT 65
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 235 TGAATGCGCTCAACAGACGCTCAAAAGCTTCAGAACTTATTCATTTCTGTCTCAT 294
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 66 TCTCATGCGCTCCTGCTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 107
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 295 CTTAATATGCTCTTCTGCTGATTTGATTTGATTTGATTTGATTTGATTTGATTTCT 336
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

RESULT 5

```

US-09-949-016-13181
; Sequence 13181, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13181
; LENGTH: 16062
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13181
```

```

Query Match          42.6%; Score 46; DB 4; Length 16062;
Best Local Similarity 65.7%; Pred. No. 1.7e-05;
Matches 67; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
```

```

QY 6 TGAGAGAAAGGCTCAGGCGCAGGAGCAAGCTCCAGAAATGCTTTCATTTGTTCTGAT 65
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 12661 TGAATGCGCTCAACAGACGCTCAAAAGCTTCAGAACTTATTCATTTCTGTCTCAT 12720
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 66 TCTCATGCGCTCCTGCTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 107
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 12721 CTTAATATGCTCTTCTGCTGATTTGATTTGATTTGATTTGATTTGATTTGATTTCT 12762
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

RESULT 6

```

US-09-124-671-26
; Sequence 26, Application US/09124671A
```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using bw model

Run on: July 7, 2005, 09:22:55 ; Search time 260.444 Seconds
(without alignments)
2603.465 Million cell updates/sec

Title: US-10-724-532-3

Perfect score: 108

Sequence: 1 atcgatgagagagagccctca.....gcatatcgcatgctctcg 108

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 6330943 seqs, 3139157217 residues

Total number of hits satisfying chosen parameters: 12661886

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Published Applications_NA.*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq:*
20: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq:*
21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq:*
22: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq:*
24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the change being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	108	100.0	108	20	US-10-724-532-3
2	108	100.0	108	20	US-10-724-532-4
3	108	100.0	135	20	US-10-724-532-5
4	108	100.0	135	20	US-10-724-532-6
5	50.8	47.0	159	15	US-10-371-101-9
6	50.8	47.0	159	15	US-10-371-101-13
7	46	42.6	159	19	US-10-691-412-1

8	46	42.6	525	10	US-09-918-995-4045	Sequence 4045, Ap
9	46	42.6	1635	10	US-09-873-367C-162	Sequence 162, App
10	46	42.6	1535	21	US-10-843-641A-162	Sequence 162, App
11	45	41.7	380	10	US-09-918-995-3950	Sequence 3950, Ap
12	45	41.7	418	10	US-09-918-995-5235	Sequence 5235, Ap
13	44.4	41.1	394	10	US-09-918-995-4217	Sequence 4217, Ap
14	44.4	41.1	487	10	US-09-918-995-5377	Sequence 5377, Ap
15	43.6	40.4	315	20	US-10-815-514-26	Sequence 26, Appl
16	43.6	40.4	315	20	US-10-877-990-26	Sequence 26, Appl
17	43.6	40.4	315	21	US-10-873-554-26	Sequence 26, Appl
18	41.2	38.1	407	10	US-09-918-995-3842	Sequence 3842, Ap
19	38	35.2	492	10	US-09-918-995-17377	Sequence 17377, A
20	32.8	30.4	652	11	US-09-969-034-4348	Sequence 4348, A
21	32.8	30.4	1896	21	US-10-723-518-2	Sequence 2, Appl1
22	32.8	30.4	2419	10	US-09-814-353-20506	Sequence 20506, A
23	32.8	30.4	3647	17	US-10-172-118-1260	Sequence 1260, Ap
24	32.8	30.4	3647	18	US-10-342-887-1260	Sequence 1260, Ap
25	32.8	30.4	3647	21	US-10-848-755A-148	Sequence 148, App
26	32.8	30.4	3748	9	US-09-925-301-80	Sequence 80, Appl
27	32.8	30.4	3925	20	US-10-723-860-4598	Sequence 4598, Ap
28	32.8	29.6	6481	15	US-10-037-270-1076	Sequence 1076, Ap
29	32	29.6	6481	17	US-10-117-722-1076	Sequence 1076, Ap
30	32	29.6	10625	9	US-09-727-384-5	Sequence 5, Appl1
31	32	29.6	10625	14	US-10-023-219-3	Sequence 3, Appl1
32	32	29.6	10625	21	US-10-690-276-3	Sequence 3, Appl1
33	31.8	29.4	2180	18	US-10-425-114-557	Sequence 557, App
34	31.8	29.4	2220	20	US-10-425-115-167740	Sequence 167740, A
35	30.4	28.1	613	19	US-10-767-701-25701	Sequence 25701, A
36	30.4	28.1	1938	13	US-10-087-192-740	Sequence 740, App
37	30.4	28.1	2175	9	US-09-994-485-3	Sequence 3, Appl1
38	30.4	28.1	2175	9	US-09-832-292-7	Sequence 7, Appl1
39	30.2	28.0	639	21	US-10-470-048B-40	Sequence 40, Appl
40	30	27.8	415	9	US-09-864-761-3336	Sequence 3336, Ap
41	30	27.8	1269	19	US-10-767-705-1475	Sequence 1475, Ap
42	29.8	27.6	1137	19	US-10-437-963-88641	Sequence 88641, A
43	29.8	27.6	113306	17	US-10-292-798-1007	Sequence 1007, App
44	29.8	27.6	251199	21	US-10-482-029-205	Sequence 205, App
45	29.6	27.4	605	13	US-10-027-632-238890	Sequence 238890, A

ALIGNMENTS

RESULT 1
US-10-724-532-3
; Sequence 3, Application US/10724532
; Publication No. US20040203027A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Thomas D
; TITLE OF INVENTION: Signal for Targeting Molecules to the Sarc(endo)plasmic
; FILE REFERENCE: SR RPA
; CURRENT APPLICATION NUMBER: US/10/724.532
; PRIOR FILING DATE: 2003-11-29
; PRIOR APPLICATION NUMBER: US 60/430322
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 3
; LENGTH: 108
; TYPE: DNA
; ORGANISM: mus musculus
US-10-724-532-3

Query Match 100.0%; Score 108; DB 20; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.3e-26;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCAATGAGAGAGGCTCAGGAGGAGAACTCCGAAATGCTTATTCCTTTTGT 60
DB 1 ATGCAATGAGAGAGGCTCAGGAGGAGAACTCCGAAATGCTTATTCCTTTTGT 60
QY 61 CTGATTCATCTGCTCTGCTGATTTGCAATTATGTCATGCTCTG 108

Db 61 CTGATTCATCTGCTCTCTGCTATTTGATTAATCGTCATGCTCTCTG 108

RESULT 2
US-10-724-532-4/c
; Sequence 4, Application US/10724532
; Publication No. US20040203027A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Thomas D
; TITLE OF INVENTION: Signal for Targeting Molecules to the Sarco(endo)plasmic
; FILE REFERENCE: SR RPA
; CURRENT APPLICATION NUMBER: US/10/724,532
; CURRENT FILING DATE: 2003-11-29
; PRIOR APPLICATION NUMBER: US 60/430322
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 108
; TYPE: DNA
; ORGANISM: mus musculus
US-10-724-532-4

Query Match 100.0%; Score 108; DB 20; Length 108;
Best Local Similarity 100.0%; Pred. No. 1,3e-26;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCATGAGAGAGGCTCTCAGGCCAGGCAAACTCCAGAAATGCTTTATGCTTTTGT 60
|||
Db 108 ATGCATGAGAGAGGCTCTCAGGCCAGGCAAACTCCAGAAATGCTTTATGCTTTTGT 49
CTGATTCATCTGCTCTCTGCTATTTGATTAATCGTCATGCTCTCTG 108
48 CTGATTCATCTGCTCTCTGCTATTTGATTAATCGTCATGCTCTCTG 1

RESULT 3
US-10-724-532-5
; Sequence 5, Application US/10724532
; Publication No. US20040203027A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Thomas D
; TITLE OF INVENTION: Signal for Targeting Molecules to the Sarco(endo)plasmic
; FILE REFERENCE: SR RPA
; CURRENT APPLICATION NUMBER: US/10/724,532
; CURRENT FILING DATE: 2003-11-29
; PRIOR APPLICATION NUMBER: US 60/430322
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 135
; TYPE: DNA
; ORGANISM: mus musculus
US-10-724-532-5

Query Match 100.0%; Score 108; DB 20; Length 135;
Best Local Similarity 100.0%; Pred. No. 1,4e-26;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCATGAGAGAGGCTCTCAGGCCAGGCAAACTCCAGAAATGCTTTATGCTTTTGT 60
|||
Db 13 ATGCATGAGAGAGGCTCTCAGGCCAGGCAAACTCCAGAAATGCTTTATGCTTTTGT 72
CTGATTCATCTGCTCTCTGCTATTTGATTAATCGTCATGCTCTCTG 108
73 CTGATTCATCTGCTCTCTGCTATTTGATTAATCGTCATGCTCTCTG 120

RESULT 4

US-10-724-532-6/c
; Sequence 6, Application US/10724532
; Publication No. US20040203027A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Thomas D
; TITLE OF INVENTION: Signal for Targeting Molecules to the Sarco(endo)plasmic
; FILE REFERENCE: SR RPA
; CURRENT APPLICATION NUMBER: US/10/724,532
; CURRENT FILING DATE: 2003-11-29
; PRIOR APPLICATION NUMBER: US 60/430322
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 135
; TYPE: DNA
; ORGANISM: mus musculus
US-10-724-532-6

Query Match 100.0%; Score 108; DB 20; Length 135;
Best Local Similarity 100.0%; Pred. No. 1,4e-26;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCATGAGAGAGGCTCTCAGGCCAGGCAAACTCCAGAAATGCTTTATGCTTTTGT 60
|||
Db 123 ATGCATGAGAGAGGCTCTCAGGCCAGGCAAACTCCAGAAATGCTTTATGCTTTTGT 64
CTGATTCATCTGCTCTCTGCTATTTGATTAATCGTCATGCTCTCTG 108
61 CTGATTCATCTGCTCTCTGCTATTTGATTAATCGTCATGCTCTCTG 107
63 CTGATTCATCTGCTCTCTGCTATTTGATTAATCGTCATGCTCTCTG 16

RESULT 5
US-10-371-101-9
; Sequence 9, Application US/10371101
; Publication No. US2003014995A1
; GENERAL INFORMATION:
; APPLICANT: Zwaal, Richard
; APPLICANT: Groenen, Jose
; APPLICANT: Bogaert, Thierry
; TITLE OF INVENTION: COMPOUND SCREENING METHODS
; FILE REFERENCE: D00590.70035.US
; CURRENT APPLICATION NUMBER: US/10/371,101
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: GB 9908670.4
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: US 60/129,596
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: GB 9912736.7
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: 09/549,872
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 159
; TYPE: DNA
; ORGANISM: Sus sp.
US-10-371-101-9

Query Match 47.0%; Score 50.8; DB 15; Length 159;
Best Local Similarity 68.6%; Pred. No. 3,8e-07;
Matches 70; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

Qy 6 TGAAGAGAGGCTCTCAGGCCAGGCAAACTCCAGAAATGCTTTATGCTTTTGT 65
|||
Db 54 TGAATGCTCTAAAGAGAGGCTCTCAGGCCAGGCAAACTCCAGAAATGCTTTATGCTTTTGT 113
TCTATCTGCTCTCTGCTATTTGATTAATCGTCATGCTCTCTG 107
114 CTATATATGCTCTCTGCTATTTGATTAATCGTCATGCTCTCTG 155

Query Match	48.5%	Score 52.4;	DB 4;	Length 858;
Best Local Similarity	69.6%	Pred. No. 2.2e-06;		
Matches	71;	Conservative	0;	Mismatches 31;
			Indels	0;
			Gaps	0;

Qy	2	AGGACCATGACGATATATGCAAAATTCAGCAGGACATGAGATTCAGACAAAGAAGCAATG	61
Db	678	AGAACCATGACGATATGTCAGATCAGCAGAGACATATCAAGATGAGACAGAAATTGATA	61.9
Qy	62	AAAGCATTTGGAGGTTTCGCTCGGCTGAGAGGCTTCTCTCA	103
Db	618	AATAGCTTCTGAGGTTTTCAGCTGGCTTGTGTGGGCATTTCA	577

RESULT 2			
OCPEHAM/c			
LOCUS	2841 bp	mRNA	
DEFINITION	O.cuniculus mRNA for phospholamban.		
		linear	MAM 24-JUL-1992

VERSION	Y00761.1	GI:1661
KEYWORDS	phospholamban.	
SOURCE	Oryctolagus cuniculus (rabbit)	

ORGANISM *Oryctolagus cuniculus*

REFERENCE

1 (bases 1 to 2841)

Euryarchaea; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

AUTHORS	TITLE
Fujii, J., Lytton, J., Tada, M. and MacLennan, D.H.	Rabbit cardiac and slow-twitch muscle express the same

phospholamban gene
FEBS Lett. 227 (1), 51-55 (1988)

MEDLINE 8811222
PUBMED 2962883

FEATURES	Location/Qualifiers
SOURCE	1. .2841

CDS

```

Location/Qualifiers
1..2841
/organism="Oryctolagus cuniculus"
/mol_type="mRNA"
/db_xref="taxon:9986"
178..336
/codon_start=1
/product="phospholamban"
/protein_id="CAA68730.1"
/db_xref="GI:1662"
/db_xref="GCA:P20006"
/db_xref="UniProt/Swiss-Prot:P20006"
/translation="MEKQYLTIRSAIRRASTIEPQQAQNQLNLFINCLLIICLL
ICIIYML"

```

ORIGIN

Query Match	48.5%	Score 52.4;	DB 4;	Length 2841;
Best Local Similarity	69.6%	Pred. No. 2.5e-06;		
Matches	71;	Conservative	0;	Mismatches 31;
			Indels	0;
			Gaps	0

QY 2 AGGAGCATACGATATGTGCAAAATCACAGAGGCAGTGTGATTCAGACAAAAAGCAATG 61
Db 332 AGAACATTCACGATGATGCAAGTACACAGSAGACATTCAGATGTAGACAGAAATTGATA 273
QY 62 AAAGCATTTGGAGGTTCTGCCTGGCCTGAAGCCTTCTCTCA 103
Db 212 AATAGGTTCTGAGAGTTTGAACCTGCTGTGTGGAGCATTTCA 231

RESULT 3
BD247907/c

LOCUS	BD247997	159 bp	DNA	linear	PAT 17-JUL-2003
DEFINITION	Method for screening compounds.				
ACCESSION	BD247997				

ACCESSION	BD247907
VERSION	BD247907.1 GI:33057677
KEYWORDS	JP 2002541859-A/9

RECORDS OF 2002
SOURCE Sus BP.

ORGANISM

REFERENCE
1 (bases 1 to 159)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

AUTHORS Zwaal, R., Groenen, J. and Bogaert, T.
TITLE Method for screening compounds
JOURNAL Patent: JP 2002541859-A 9 10-DEC-2002;
SEARCHED YES

COMMENT

OS	Sus sp. (pig)	
PN	JP 2002541859-A/9	
PD	10-DEC-2002	
PR	14-APR-2000 JP 2000612503	
PP	15-APR-1999 GB 9908670.4,15-APR-1999 US	60/129596 PR
P1	01-JUN-1999 GB 9912736.7	
PI	RICHARD ZWAAL,JOSE GROENEN,THIERRY BOGAERT	
PC	C12Q1/42, C12N15/09, C12Q1/02, C12N15/00	
CC	Method for screening compounds	
FM	Key	
FT	Location/Qualifiers	
TT	source	
	1.159	
	/organism='Sus sp. (pig)'	

FEATURES	Location/Qualifiers
source	1. .159

```
/mol_type="genomic DNA"  
/db_xref="taxon:9826"
```

ORIGIN

Query Match	47.0%	Score 50.8	DB 6	Length 159;
Best Local Similarity	68.6%	Pred. No. 6e-06;		
Matches	70;	Conservative	0;	Mismatches 32; Indels 0; Gaps 0;

QY 2 AGAGGCAATGACGATTAATGCAAAATCAGAGAGGCACATGGAATTCGACAAAAGCAATG 61
Db 155 AGAAGCATCAAGATGATGCATAATCAGCAGAGGCAATTTAAGATGAGACAGAAATTGATA 96
QY 62 AAAGCATTTGAGAGGTTCTGCGCTGAGGCGCTGAGGCGCTTCTCTCA 103
Db 95 AATAGTTCTGAAAGGTTTGAACGCTGTTGTAGGCAATTTCA 54

RESULT 4
BD247911/C
150 4- 14:00:00 DATE 17-MAR-2003

LOCUS
DEFINITION

ACCESSION	BD247511
VERSION	BD247911.1 GI:33057681
KEYWORDS	JP 2002541859-A/13.

SOURCE ORGANISM

other sequences; artificial sequences.

REFERENCE	1 (bases 1 to 159)
AUTHORS	Zwaal, R., Groenen, J. and Bogaert, T.

TITLE	Method for screening compounds
JOURNAL	Patent: JP 2002541859-A 13 10-DEC-2002,

CONCLUSIONS

```

OS Artificial Sequence
PN JP 2002541859-A/13
PD 10-DEC-2002
PF 14-APR-2002 JP 2000612503
PR 15-APR-1999 GB 9908670.4,15-APR-1999 US 60/129596 PR
PI 01-JUN-1999 GB 9912738.7
PI RICHARD ZWAAL,JOHN GROENEN,THIERRY BOGAERT
PC C12Q01/42,C12N15/09,C12Q01/92,C12N15/00
CC Description of Artificial Sequence:HUMANIZED PIG PLB CDNA FR
Key Location/Qualifiers
FT source 1..159
FT 1..159/organism='Artificial Sequence'.

```

FEATURES
source

```

/mol_type="genomic DNA"
/db_xref="taxon:32630"

```

ORIGIN

Query Match	47.0%;	Score 50.8;	DB 6;	length 159;
Best Local Similarity	68.6%;	Pred. No. 6e-06;		
Matches 70;	Conservative 0;	Mismatches 32;	Indels 0;	Gaps 0;

[illegible]

CC methods can be used to identify compounds for use in the treatment of
CC some muscle pathologies, cardiac hypertrophy, heart failure,
CC hypertension, diabetes, Darier-White disease and Brody's disease
XX

Sequence 159 BP, 45 A; 41 C; 22 G; 51 T; 0 U; 0 Other;

Query Match 47.0%; Score 50.8; DB 3; Length 159;
Best Local Similarity 68.6%; Pred. No. 3.3e-06;
Matches 70; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 2 AGAGCATGACGATATGCAATTCAGCAGAGCGCAGATGACGACAAAGCAATG 61
DB 155 AGAAGCATGACGATATGCAATTCAGCAGAGCGCAGATGACGACAAAGCAATG 96

QY 62 AAAGCATCTGAGGTTCTGCTGCGCTGAGGCGCTTCTCTCA 103
DB 95 AATAGCTTCTGAGGTTCTGAGGTTCTGAGGCGCTTCTCTCA 54

RESULT 2

ADBS3082/C
ID ADBS3082 standard; DNA; 701 BP.

AC ADBS3082;

DT 04-DEC-2003 (first entry)

DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3624.

KW toxic effect; gene expression profile; hepatotoxicity; diagnostic marker;
KW toxicity marker; toxicity progression; drug screening;
KW primary rat hepatocyte toxicity modelling; gene; db.

OS Rattus norvegicus.

PN W02003065993-A2.

PD 14-AUG-2003.

PF 04-FEB-2003; 2003WO-US003482.

PR 04-FEB-2002; 2002US-0353171P.

PR 13-MAR-2002; 2002US-0363534P.

PR 08-APR-2002; 2002US-0370248P.

PR 10-APR-2002; 2002US-0371134P.

PR 10-APR-2002; 2002US-0371135P.

PR 10-APR-2002; 2002US-0371150P.

PR 11-APR-2002; 2002US-0371413P.

PR 19-APR-2002; 2002US-0373601P.

PR 12-APR-2002; 2002US-0374139P.

PR 08-MAY-2002; 2002US-0378370P.

PR 09-MAY-2002; 2002US-0378652P.

PR 09-MAY-2002; 2002US-0378653P.

PR 09-MAY-2002; 2002US-0394230P.

PR 09-JUL-2002; 2002US-0394253P.

PR 04-SEP-2002; 2002US-0407688P.

PR 28-JAN-2003; 2003US-0442900P.

XX (GENE-) GENE LOGIC INC.

XX Mendrick D, Porter M, Johnson K, Higgs B, Castle A, Orr M;

PI Elshof M;

XX WPI; 2003-731472/69.

XX Determining if a compound induces a toxic effect on a tissue or cell, for
XX identifying hepatotoxic compounds, comprises comparing a gene expression
XX profile of a tissue or cell sample to a database of Tox mean and non-Tox
XX mean values.

PS Claim 44; SEQ ID NO 3624; 874bp; English.

XX The present invention describes a method for determining whether a
CC compound induces a toxic effect on a tissue or cell. The method comprises
CC preparing a gene expression profile of a tissue or cell sample exposed to
CC the compound, and comparing the gene expression profile to a database
CC comprising data or information on the Tox mean and non-Tox mean value.
CC The method is useful for predicting or identifying at least one toxic
CC effect, particularly hepatotoxicity, of a test or unknown compound. The
CC genes listed in the specification are useful as diagnostic or toxicity
CC markers for the prediction or identification of the physiological state
CC of tissue or cell sample that has been exposed to a compound, or to
CC identify or predict the toxic effects of a compound or an agent. These
CC may also be used as markers for monitoring toxicity progression or for
CC drug screening. The present sequence represents a primary rat hepatocyte
CC toxicity modelling related gene sequence from the present invention.

Sequence 701 BP, 184 A; 178 C; 141 G; 198 T; 0 U; 0 Other;

Query Match 46.5%; Score 50.2; DB 10; Length 701;
Best Local Similarity 68.0%; Pred. No. 8.1e-06;
Matches 70; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 1 CAGAGCATGACGATATGCAATTCAGCAGAGCGCAGATGACGACAAAGCAAT 60

DB 329 CAGAGCATGACGATATGCAATTCAGCAGAGCGCAGATGACGACAAAGCAAT 270

QY 61 GAAGCATCTGAGGTTCTGCTGCGCTGAGGCGCTTCTCTCA 103

DB 269 AAAGGTTCTGAGGTTCTGAGGTTCTGAGGCGCTTCTCTCA 227

RESULT 3

ADR97285/C
ID ADR97285 standard; DNA; 159 BP.

AC ADR97285;

DT 16-DEC-2004 (first entry)

DE Human phospholamban polymorphism fragment DNA.

KW ds; human; phospholamban; polymorphism; cardiovascular disease.

OS Homo sapiens.

PN US2004191802-A1.

PD 30-SEP-2004.

PF 22-OCT-2003; 2003US-00691412.

PR 22-OCT-2002; 2002US-0420295P.

XX (KRANV/) KRANTAS B G.

XX (HAGH/) HAGHIGHI K.

XX Kranias EG, Haghighi K;

XX WPI; 2004-689841/67.

XX Phospholamban polymorphism assessment in individual, for determining risk
XX for developing cardiovascular disease, by comparing analysis of the
XX nucleotide fragment with a predetermined phospholamban nucleotide
XX fragment sequence.

PS Claim 15; SEQ ID NO 1; 15bp; English.

XX The invention relates to a method of phospholamban polymorphism
XX assessment in an individual which comprises comparing the analysis of the
XX nucleotide fragment with a predetermined phospholamban nucleotide
XX fragment sequence to determine whether the individual carries a
XX phospholamban polymorphism. The methods and phospholamban polymorphism
XX fragment are useful for determining if an individual is at risk for

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Comugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 7, 2005, 09:02:25 ; Search time 1353.33 Seconds

(without alignments)
3037.641 Million cell updates/sec

Title: US-10-724-532-4

Perfect score: 108

Sequence: 1 caggagcatgacgataatgc.....tgaggctctctcatgcat 108

Scoring table: IDENTITY NUC

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: gb_ests1:*
2: gb_ests2:*
3: gb_hic:*
4: gb_ests3:*
5: gb_ests4:*
6: gb_ests5:*
7: gb_ests6:*
8: gb_gsa1:*
9: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	50.8	47.0	381	5	BX669692 BX669692
C 2	50.8	47.0	702	5	BX922974 BX922974
C 3	50.8	47.0	724	5	BX674983 BX674983
C 4	50.8	47.0	740	5	BX924154 BX924154
C 5	50.8	47.0	758	5	BX923697 BX923697
C 6	50.8	47.0	811	7	CK449263 CK449263
C 7	50.2	46.5	179	2	BE113353 BE113353
C 8	50.2	46.5	377	2	BF547332 BF547332
C 9	50.2	46.5	417	1	AI322542 AI322542
C 10	50.2	46.5	439	2	BE115006 BE115006
C 11	50.2	46.5	449	2	BE098177 BE098177
C 12	50.2	46.5	449	2	BE098177 BE098177
C 13	50.2	46.5	451	4	BI288911 BI288911
C 14	50.2	46.5	454	4	BE099930 BE099930
C 15	50.2	46.5	476	2	BF525258 BF525258
C 16	50.2	46.5	480	7	CR471116 CR471116
C 17	50.2	46.5	487	4	BG379827 BG379827
C 18	50.2	46.5	498	1	AI603160 AI603160
C 19	50.2	46.5	511	4	BF395370 BF395370
C 20	50.2	46.5	513	4	BI296789 BI296789
C 21	50.2	46.5	518	2	BE112568 BE112568
C 22	50.2	46.5	527	2	BF395607 BF395607
C 23	50.2	46.5	528	2	BF395670 BF395670
C 24	50.2	46.5	540	2	BF395398 BF395398

C 25	50.2	46.5	575	4	BI290034 BI290034
C 26	50.2	46.5	589	2	BF525010 BF525010
C 27	50.2	46.5	608	1	AI103929 AI103929
C 28	50.2	46.5	699	7	CK358482 CK358482
C 29	50.2	46.5	710	7	CK359590 CK359590
C 30	50.2	46.5	718	7	CK358464 CK358464
C 31	50.2	46.5	719	7	CK356296 CK356296
C 32	50.2	46.5	731	7	CK357243 CK357243
C 33	50.2	46.5	737	7	CK357232 CK357232
C 34	50.2	46.5	738	7	CK355359 CK355359
C 35	50.2	46.5	738	7	CK357123 CK357123
C 36	50.2	46.5	744	7	CK356439 CK356439
C 37	50.2	46.5	744	7	CK357747 CK357747
C 38	50.2	46.5	745	7	CK355314 CK355314
C 39	50.2	46.5	745	7	CK356371 CK356371
C 40	50.2	46.5	748	7	CK359219 CK359219
C 41	50.2	46.5	754	7	CK355445 CK355445
C 42	50.2	46.5	758	7	CK355453 CK355453
C 43	50.2	46.5	758	7	CK357746 CK357746
C 44	50.2	46.5	762	7	CK359188 CK359188
C 45	50.2	46.5	764	7	CK357447 CK357447

ALIGNMENTS

RESULT 1	BX669692/c	381 bp	mRNA	linear	EST 07-MAY-2004
LOCUS	BX669692	Sus scrofa library (scac)	Sus scrofa	CDNA clone	
DEFINITION	scac00281.c.02 5prim, mRNA sequence.				
ACCESSION	BX669692				
VERSION	BX669692.1	GI:37979481			
KEYWORDS	EST				
SOURCE	Sus scrofa (pig)				
ORGANISM	Sus scrofa				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.				
AUTHORS	1 (bases 1 to 381)				
TITLE	Soares, M., Bonaldo, F., and Hately, F.				
JOURNAL	A Pig Normalised Multi-Tissue cDNA Library				
COMMENT	Unpublished (2003)				
	Contact: Tosser-Klopp G				
	Genetique Animale				
	Institut National de la Recherche Agronomique				
	Chemin de Borde-Rouge - Auzeville BP27, 31326 Castanet-Tolosan cedex, FRANCE				
	Tel: 33 (0) 5.61.28.51.14				
	Fax: 33 (0) 5.61.28.53.08				
	Email: tosser@toulouse.inra.fr				
	Sequence cleaned of vector, adaptor and repetitions. Contact us at sigenastupport@journ.inra.fr to obtain the chromatogram of this sequence.				
FEATURES	Plate: 0028	row: C	column: 2.		
source	Location/Qualifiers				
	1..381				
	/organism="Sus scrofa"				
	/mol_type="mRNA"				
	/db_xref="taxon:9823"				
	/clone="scac00281.c.02"				
	/tissue_type="mixed"				
	/clone_lib="Sus Scrofa library (scac)"				
	/note="Vector: pTRIP-pac vector; tissues: adipose tissue, brain, kidney, liver, muscle, ovary, testis, heart, hypothalamus, pancreas, skin, spleen, thymus, placenta, pituitary gland, seminal vesicle, small intestine, uterus, adrenals, bulbo uretral gland, cerebral trunk, epididymis, female gonad, gall-bladder, hippocampus, large intestine, male gonad, melanocytes, stomach, udder"				
ORIGIN					
Query Match	47.0%;	Score 50.8;	DB 5;	Length 381;	

Best Local Similarity 68.6%; Pred. No. 0.00012;
Matches 70; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 2 AGGAGCATGACGATGATGCAATTCAGCGAGGAGGAGATGAGAAATCAGCAAAAGCAATG 61
DB 183 AGAAGCATCAGCATGATGCAAAATCAGCAAGGAGCATATTAAGATGAGCAGAAATTGATA 124
QY 62 AAGAGATTCTGAGGTTCTGCGCTGAGGAGGCTTCTCA 103
DB 123 AATAGGTTCTGAAGGTTTGACGTCGCTTTGAGGCAATTCA 82

RESULT 2
BX922974/c 702 bp mRNA linear EST 07-MAY-2004
LOCUS BX922974 Sus Scrofa library (scan) Sus scrofa cDNA clone
DEFINITION scan0013d.f.14 5prim, mRNA sequence.

ACCESSION BX922974
VERSION BX922974.1 GI:41139822
KEYWORDS EST.

Sus scrofa (pig)

ORGANISM

Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE 1 (bases 1 to 702)
Bonnet, A., Tosser-Klopp, G., Benne, F., Cabau, C., Villegier, S.,
Soares, M., Bonaldo, F. and Hately, F.

A Pig Normalised Multi-Tissue cDNA Library
Unpublished (2003)
Contact: Tosser-Klopp G
Genetique Animale
Institut National de la Recherche Agronomique
Chemin de Borde-Rouge - Auzeville BP27, 31326 Castanet-Tolosan
cedex, FRANCE
Tel: 33 (0) 5.61.28.51.14
Fax: 33 (0) 5.61.28.53.08
Email: tosser@toulouse.inra.fr
Sequence cleaned of vector, adaptor and repetitions. Contact us
at sigenastupport@jouy.inra.fr to obtain the chromatogram of this
sequence.

Plate: 0013 row: j column: 14.

Location/Qualifiers

FEATURES

source

1..702

/organism="Sus scrofa"

/mol_type="mRNA"

/db_xref="taxon:9823"

/clone="scan0013d.f.14"

/tissue_type="mixed"

/dev_stage="from embryos to adults"

/clone_lib="Sus Scrofa library (scan)"

/note="Tissues: adipose tissue, brain, kidney, liver,
muscle, ovary, testis, heart, hypothalamus, pancreas,
skin, spleen, thymus, placenta, pituitary gland, seminal
vesicle, small intestine, uterus, adrenals, bulbo urethral
gland, cerebral trunk, epididymis, female gonad,
gall-bladder, hippocampus, large intestine, male gonad,
melanocytes, stomach, udder"

ORIGIN

Query Match 47.0%; Score 50.8; DB 5; Length 702;
Best Local Similarity 68.6%; Pred. No. 0.00013;
Matches 70; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 2 AGGAGCATGACGATGATGCAATTCAGCGAGGAGGAGATGAGAAATCAGCAAAAGCAATG 61
DB 317 AGAAGCATCAGCATGATGCAAAATCAGCAAGGAGCATATTAAGATGAGCAGAAATTGATA 258

QY 62 AAGAGATTCTGAGGTTCTGCGCTGAGGAGGCTTCTCA 103
DB 257 AATAGGTTCTGAAGGTTTGACGTCGCTTTGAGGCAATTCA 216

RESULT 3

BX674983/c 724 bp mRNA linear EST 07-MAY-2004
LOCUS BX674983 Sus Scrofa library (scan) Sus scrofa cDNA clone
DEFINITION scan0039f.h.23 5prim, mRNA sequence.

ACCESSION BX674983
VERSION BX674983.1 GI:38008935
KEYWORDS EST.

Sus scrofa (pig)

ORGANISM

Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE 1 (bases 1 to 724)
Bonnet, A., Tosser-Klopp, G., Benne, F., Cabau, C., Villegier, S.,
Soares, M., Bonaldo, F. and Hately, F.

A Pig Normalised Multi-Tissue cDNA Library
Unpublished (2003)
Contact: Tosser-Klopp G
Genetique Animale
Institut National de la Recherche Agronomique
Chemin de Borde-Rouge - Auzeville BP27, 31326 Castanet-Tolosan
cedex, FRANCE
Tel: 33 (0) 5.61.28.51.14
Fax: 33 (0) 5.61.28.53.08
Email: tosser@toulouse.inra.fr
Sequence cleaned of vector, adaptor and repetitions. Contact us
at sigenastupport@jouy.inra.fr to obtain the chromatogram of this
sequence.

Plate: 0039 row: h column: 23.

Location/Qualifiers

FEATURES

source

1..724

/organism="Sus scrofa"

/mol_type="mRNA"

/db_xref="taxon:9823"

/clone="scan0039f.h.23"

/tissue_type="mixed"

/clone_lib="Sus Scrofa library (scan)"

/note="Vector: pT7SD-pec vector; tissues: adipose tissue,
brain, kidney, liver, muscle, ovary, testis, heart,
hypothalamus, pancreas, skin, spleen, thymus, placenta,
pituitary gland, seminal vesicle, small intestine,
uterus, adrenals, bulbo urethral gland, cerebral trunk,
epididymis, female gonad, gall-bladder, hippocampus,
large intestine, male gonad, melanocytes, stomach, udder"

ORIGIN

Query Match 47.0%; Score 50.8; DB 5; Length 724;
Best Local Similarity 68.6%; Pred. No. 0.00013;
Matches 70; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 2 AGGAGCATGACGATGATGCAATTCAGCGAGGAGGAGATGAGAAATCAGCAAAAGCAATG 61
DB 318 AGAAGCATCAGCATGATGCAAAATCAGCAAGGAGCATATTAAGATGAGCAGAAATTGATA 279

QY 62 AAGAGATTCTGAGGTTCTGCGCTGAGGAGGCTTCTCA 103
DB 278 AATAGGTTCTGAAGGTTTGACGTCGCTTTGAGGCAATTCA 237

RESULT 4

BX924154/c 740 bp mRNA linear EST 07-MAY-2004
LOCUS BX924154 Sus Scrofa library (scan) Sus scrofa cDNA clone
DEFINITION scan0011d.f.23 5prim, mRNA sequence.

ACCESSION BX924154
VERSION BX924154.1 GI:41141002
KEYWORDS EST.

Sus scrofa (pig)

ORGANISM

Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE 1 (bases 1 to 740)
Bonnet, A., Tosser-Klopp, G., Benne, F., Cabau, C., Villegier, S.,
Soares, M., Bonaldo, F. and Hately, F.

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 7, 2005, 09:02:25 ; Search time 61.7778 Seconds
(without alignments)
2860.541 Million cell updates/sec

Title: US-10-724-532-4

Perfect score: 108

Sequence: 1 caggcgcacgcacacacacgc.....tgaggcctctctcatgcac 108

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 1202784 seqs, 81813359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/prodata/1/ina/5A_COMB.seq:*
- 2: /cgn2_6/prodata/1/ina/5B_COMB.seq:*
- 3: /cgn2_6/prodata/1/ina/6A_COMB.seq:*
- 4: /cgn2_6/prodata/1/ina/6B_COMB.seq:*
- 5: /cgn2_6/prodata/1/ina/PCTUS_COMB.seq:*
- 6: /cgn2_6/prodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	50.8	47.0	159	4 US-09-549-872B-9	Sequence 9, Appl
C 2	50.8	47.0	159	4 US-09-549-872B-13	Sequence 13, Appl
C 3	46	42.6	480	4 US-09-513-999C-10799	Sequence 10799, A
C 4	46	42.6	1635	4 US-09-949-016-1439	Sequence 1439, Ap
C 5	46	42.6	16062	4 US-09-949-016-13181	Sequence 13181, A
C 6	43.6	40.4	315	3 US-09-124-671-26	Sequence 26, Appl
C 7	32	29.6	6481	4 US-09-620-312D-1076	Sequence 1076, Ap
C 8	30.4	28.1	2175	4 US-08-914-999-3	Sequence 3, Appl
C 9	30.2	28.0	74353	4 US-09-949-016-15336	Sequence 15336, A
C 10	29	26.9	474	4 US-09-513-999C-1161	Sequence 1161, Ap
C 11	29	26.9	1123	3 US-09-188-930-28	Sequence 28, Appl
C 12	29	26.9	1123	3 US-09-188-930-203	Sequence 203, Appl
C 13	29	26.9	1123	3 US-09-312-283C-28	Sequence 28, Appl
C 14	29	26.9	1123	3 US-09-312-283C-203	Sequence 203, Appl
C 15	28.8	26.7	879	4 US-09-489-039A-5041	Sequence 5041, Ap
C 16	28.8	26.3	162914	4 US-09-949-016-15578	Sequence 15578, A
C 17	27.8	25.7	72	3 US-08-945-734-11	Sequence 11, Appl
C 18	27.8	25.7	72	3 US-09-258-797-11	Sequence 11, Appl
C 19	27.8	25.7	72	5 PCT-US96-09451-11	Sequence 11, Appl
C 20	27.8	25.7	568	4 US-08-956-171E-999	Sequence 999, Appl
C 21	27.8	25.7	568	4 US-08-781-986A-999	Sequence 999, Appl
C 22	27.8	25.7	1920	3 US-09-160-496-4	Sequence 4, Appl
C 23	27.8	25.7	48313	4 US-09-949-016-17088	Sequence 17088, A
C 24	27.8	25.7	65424	4 US-09-949-016-12426	Sequence 12426, A
C 25	27.6	25.6	601	4 US-09-949-016-202802	Sequence 202802, A
C 26	27.6	25.6	26050	4 US-09-949-016-17449	Sequence 17449, A
C 27	27.6	25.6	98844	3 US-09-791-211-10	Sequence 10, Appl

C 28	27.6	25.6	14376	4 US-09-949-001-29	Sequence 29, Appl
C 29	27.6	25.6	144034	4 US-09-949-001-35	Sequence 35, Appl
C 30	27.4	25.4	483	4 US-09-583-110-2272	Sequence 2272, Ap
C 31	27.4	25.4	489	4 US-09-107-433-492	Sequence 492, Appl
C 32	27.4	25.4	601	4 US-09-949-016-82861	Sequence 82861, A
C 33	27.4	25.4	957	1 US-08-309-182B-1	Sequence 1, Appl
C 34	27.4	25.4	1117	4 US-09-552-225A-11	Sequence 11, Appl
C 35	27.4	25.4	1851	4 US-09-949-016-3036	Sequence 3036, Ap
C 36	27.4	25.4	2120	3 US-09-149-476-160	Sequence 160, Appl
C 37	27.4	25.4	2628	4 US-09-774-528-27	Sequence 27, Appl
C 38	27.4	25.4	8590	4 US-09-949-016-5562	Sequence 5562, Ap
C 39	27.4	25.4	10300	4 US-09-949-016-636	Sequence 636, Appl
C 40	27.4	25.4	38575	4 US-09-949-016-17304	Sequence 17304, A
C 41	27.4	25.4	119153	4 US-09-949-016-12378	Sequence 12378, A
C 42	27.4	25.4	213456	4 US-09-820-007-3	Sequence 3, Appl
C 43	27.4	25.4	323820	4 US-09-949-016-14139	Sequence 14139, A
C 44	27.2	25.2	7644	4 US-09-949-016-17610	Sequence 17610, A
C 45	27	25.0	372	4 US-09-270-767-5510	Sequence 5510, Ap

ALIGNMENTS

```

RESULT 1
US-09-549-872B-9/C
; Sequence 9, Application US/09549872B
; Patent No. 6540996
; GENERAL INFORMATION:
; APPLICANT: Zwaal, Richard
; APPLICANT: Groenen, Jose
; APPLICANT: Bogaert, Thierry
; TITLE OF INVENTION: COMPOUND SCREENING METHODS
; FILE REFERENCE: D00590/70008 (JRV/RE)
; CURRENT APPLICATION NUMBER: US/09/549, 872B
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: GB 9908670.4
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: US 60/129, 596
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: GB 9912736.7
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 159
; TYPE: DNA
; ORGANISM: Sus sp.
US-09-549-872B-9

Query Match      47.0% Score 50.8; DB 4; Length 159;
Best Local Similarity 68.6%; Pred. No. 5.6e-08;
Matches 70; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY
2 AGACATGATGATATGCAATATGACAGAGGACAGATGATGACAAAGCAATG 61
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 155 AGACATGATGATATGCAATATGACAGAGGACAGATGATGACAAAGCAATG 96
| | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 95 AATAGGTTCTGAAAGGTTTGAAGTCTGTTGAGGCAATTTCA 54
| | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 2
US-09-549-872B-13/C
; Sequence 13, Application US/09549872B
; Patent No. 6540996
; GENERAL INFORMATION:
; APPLICANT: Zwaal, Richard
; APPLICANT: Groenen, Jose
; APPLICANT: Bogaert, Thierry
; TITLE OF INVENTION: COMPOUND SCREENING METHODS
; FILE REFERENCE: D00590/70008 (JRV/RE)
; CURRENT APPLICATION NUMBER: US/09/549, 872B

```

CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: GB 9908670.4
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: US 60/129,596
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: GB 9912736.7
PRIOR FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 13
LENGTH: 159
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:HUMANIZED PIG
US-09-549-872B-13

Query Match 47.0%; Score 50.8; DB 4; Length 159;
Best Local Similarity 68.6%; Pred. No. 5.6e-08;
Matches 70; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 2 AGAGCATGACGATTAATGCAATTCAGCAGGAGCAGATGAGATCAGACAAAGCAATG 61
DB 155 AGAAGCATCAGATGATGCAATTCAGCAAGAGCATATTAGATGAGACAGAAATTGATA 96
QY 62 AAAGCATTTGGAGGTTCTGCTGCGCTGAGGCTTCTCTCA 103
DB 95 AATAGATTCTGAAAGGTTTGGACGTGCTTTGAGGCATTTC 54

RESULT 3

US-09-513-999C-10799/C
Sequence 10799, Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
PATENT NO. 6783961
FILE REFERENCE: 59. US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 10799
LENGTH: 480
TYPE: DNA
ORGANISM: Homo sapiens
US-09-513-999C-10799

Query Match 42.6%; Score 46; DB 4; Length 480;
Best Local Similarity 65.7%; Pred. No. 4e-06;
Matches 67; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 2 AGAGCATGACGATTAATGCAATTCAGCAGGAGCAGATGAGATCAGACAAAGCAATG 61
DB 350 AGAAGCATCAGATGATGCAATTCAGATCAGCAAGACATATTAGATGAGACAGAAATTGATA 291
QY 62 AAAGCATTTGGAGGTTCTGCTGCGCTGAGGCTTCTCTCA 103
DB 290 AATAGATTCTGAGCTTTTGAAGTGTGTTGAGGCATTTC 249

RESULT 4
US-09-949-016-1439/C
Sequence 1439, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1439
LENGTH: 1635
TYPE: DNA
ORGANISM: Human
US-09-949-016-1439

Query Match 42.6%; Score 46; DB 4; Length 1635;
Best Local Similarity 65.7%; Pred. No. 6.7e-06;
Matches 67; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 2 AGAGCATGACGATTAATGCAATTCAGCAGGAGCAGATGAGATCAGACAAAGCAATG 61
DB 336 AGAAGCATCAGATGATGCAATTCAGATCAGCAAGACATATTAGATGAGACAGAAATTGATA 277
QY 62 AAAGCATTTGGAGGTTCTGCTGCGCTGAGGCTTCTCTCA 103
DB 276 AATAGATTCTGAGCTTTTGAAGTGTGTTGAGGCATTTC 235

RESULT 5

US-09-949-016-13181/C
Sequence 13181, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13181
LENGTH: 16062
TYPE: DNA
ORGANISM: Human
US-09-949-016-13181

Query Match 42.6%; Score 46; DB 4; Length 16062;
Best Local Similarity 65.7%; Pred. No. 1.7e-05;
Matches 67; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 2 AGAGCATGACGATTAATGCAATTCAGCAGGAGCAGATGAGATCAGACAAAGCAATG 61
DB 12762 AGAAGCATCAGATGATGCAATTCAGATCAGCAAGACATATTAGATGAGACAGAAATTGATA 12703
QY 62 AAAGCATTTGGAGGTTCTGCTGCGCTGAGGCTTCTCTCA 103
DB 12702 AATAGATTCTGAGCTTTTGAAGTGTGTTGAGGCATTTC 12661

RESULT 6
US-09-124-671-26/C
Sequence 26, Application US/09124671A

Db
48 GAAAGCATTCGAGGTTCTGCGCTGAGGCTTCTCATGCAT 1

```

RESULT 2
US-10-724-532-4
; Sequence 4, Application US/10724532
; Publication No. US20040203027A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Thomas D
; TITLE OF INVENTION: Signal for Targeting Molecules to the Sarco(endo)plasmic
; TITLE OF INVENTION: Reticulum
; FILE REFERENCE: SR RPA
; CURRENT APPLICATION NUMBER: US/10/724,532
; CURRENT FILING DATE: 2003-11-29
; PRIOR APPLICATION NUMBER: US 60/430322
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 108
; TYPE: DNA
; ORGANISM: mus musculus
US-10-724-532-4

```

```

RESULT 3
US-10-724-532-5/C
; Sequence 5, Application US/10724532
; Publication NO. US20040203027A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Thomas D
; TITLE OF INVENTION: Signal for Targeting Molecules to the Sarco(endo)plasmic
; RETICULUM
; FILE REFERENCE: SR RPA
; CURRENT APPLICATION NUMBER: US/10/724,532
; CURRENT FILING DATE: 2003-11-29
; PRIOR APPLICATION NUMBER: US 60/430322
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 135
; TYPE: DNA
; ORGANISM: mus musculus
US-10-724-532-5

```

RESULT 4

```

US-10-724-532-6
; Sequence 6, Application US/10724532
; Publication No. US20040203027A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Thomas D
; TITLE OF INVENTION: Signal for Targeting Molecules to the Sarco(endo)plasmic
; TITLE OF INVENTION: Reticulum
; FILE REFERENCE: SR RPA
; CURRENT APPLICATION NUMBER: US/10/724,532
; CURRENT FILING DATE: 2003-11-29
; PRIOR APPLICATION NUMBER: US 60/430322
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 135
; TYPE: DNA
; ORGANISM: mus musculus
US-10-724-532-6

```

```

RESULT 5
US-10-371-101-9/c
; Sequence 9, Application US/10371101
; Publication No. US2003014995A1
; GENERAL INFORMATION:
; APPLICANT: Zwaal, Richard
; APPLICANT: Groenen, Joes
; APPLICANT: Bogardt, Thierry
; TITLE OF INVENTION: COMPOUND SCREENING METHODS
; FILE REFERENCE: D00590.70035_US
; CURRENT APPLICATION NUMBER: US/10/371,101
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: GB_9908670.4
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: US_60/129,596
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: GB_9912736.7
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: 09/549,872
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 159
; TYPE: DNA
; ORGANISM: Sus sp.
US-10-371-101-9

```


GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 7, 2005, 09:02:25 ; Search time 1249.17 Seconds
(without alignments)
5236.654 Million cell updates/sec

Title: US-10-724-532-5

Perfect score: 135
Sequence: 1 gagagaagctatgatcatga.....tctgtctcgagagagagag 135

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

GenBank:*
1: gb_ba:*
2: gb_hhg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pac:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_str:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52.4	38.8	858	4	RABPHLAM2
2	52.4	38.8	2841	4	OCPHLAM
3	50.8	37.6	159	6	BD247907
4	50.8	37.6	159	6	BD247911
5	50.8	37.6	159	6	AR302003
6	50.8	37.6	159	6	AR302007
7	50.8	37.6	159	6	AX040487
8	50.8	37.6	159	6	AX040491
9	50.8	37.6	737	4	SSPLB
10	50.2	37.2	159	10	S95853
11	50.2	37.2	386	10	S95849
12	50.2	37.2	701	10	RNPPLAMB
13	50.2	37.2	1786	10	RATPHLOA2
14	50.2	37.2	223728	2	AC097906
15	50.2	37.2	231910	2	AC128365
16	47.6	35.3	130240	5	BK276081
17	47.4	35.1	133901	5	BK537355
18	47	34.8	648	10	BC061097
19	47	34.8	940	10	S46792

20	47	34.8	79895	2	AC100317	AC100317 Mus muscu
21	47	34.8	177018	2	AC099716	AC099716 Mus muscu
22	46.6	34.5	3312	5	CHKPLB	M59039 Chicken car
23	46.6	34.5	3423	5	CHKPLB2	M59038 Chicken pho
24	46	34.1	306	6	CQ447405	CQ447405 Sequence
25	46	34.1	323	9	HDMPLAM	M60411 Human phosp
26	46	34.1	480	6	AX894936	AX894936 Sequence
27	46	34.1	480	6	BD030469	BD030469 Sequence
28	46	34.1	980	9	HSPLBG2	AF17764 Homo sapi
29	46	34.1	1635	6	CQ718671	CQ718671 Sequence
30	46	34.1	1635	6	AX329653	AX329653 Sequence
31	46	34.1	1635	9	HDMPLAM	M63603 Human phosp
32	46	34.1	1691	9	BC005269	BC005269 Homo sapi
33	46	34.1	60797	2	AL355356	AL355356 Homo sapi
34	46	34.1	66092	2	AL356974	AL356974 Homo sapi
35	46	34.1	150290	4	HS05914	Z99496 Human DNA s
36	44.4	32.9	314	4	AY514751	AY514751 Canis fam
37	44.4	32.9	832	4	DOGPHL	M16012 Canine card
38	44.4	32.9	832	4	DOGPLBA	M35393 Dog cardiac
39	44.4	32.9	2614	4	CEPHLX	Y00399 Dog phosphi
40	44.2	32.7	315	6	AR121629	AR121629 Sequence
41	36.2	26.8	147419	9	HS738B11	AL031736 Human DNA
42	35.6	26.4	184450	2	AC116417	AC116417 Mus muscu
43	35.2	26.1	209299	5	AC145916	AC145916 Gallus ga
44	35	25.9	5702	6	CQ719769	CQ719769 Sequence
45	35	25.9	6481	6	AR339585	AR339585 Sequence

ALIGNMENTS

RESULT 1
RABPHLAM2 858 bp DNA linear MAM 27-APR-1993
LOCUS RABPHLAM2
DEFINITION Rabbit phospholamban gene, partial exon 2.
ACCESSION M63601.1 GI:165636
VERSION
KEYWORDS phospholamban.
SEGMENT 2 of 3
SOURCE
ORGANISM Oryctolagus cuniculus (rabbit)
Oryctolagus cuniculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
REFERENCE 1 (bases 1 to 858)
AUTHORS MacLennan, D.H.
TITLE Structure of the rabbit phospholamban gene, cloning of the human cDNA, and assignment of the gene to human chromosome 6
JOURNAL J. Biol. Chem. 266 (18), 11669-11675 (1991)
MEDLINE 91268032
PUBMED 1828805
COMMENT Original source text: Rabbit DNA.
FEATURES
source
1..858
location/Qualifiers
/organism="Oryctolagus cuniculus"
/mol_type="genomic DNA"
/db_xref="taxon:9986"
/feature_1db="Rabbit genomic"
join(M63600.1:855..943,428..858)
/product="phospholamban"
428..858
/product="phospholamban"
/number=2
524..682
/function="regulatory protein of sarcoplasmic reticulum
Ca-ATPase"
/codon_start=1
/product="phospholamban"
/protein_id="AA31445.1"
/db_xref="GI:165639"
/translation="MERVQYVTRSAIRASTIEMPDQARONLQNLINFCULICLL
ICIIIVML"

ORIGIN

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using bw model

Run on: July 7, 2005, 09:02:25 ; Search time 256.389 Seconds

(without alignments)
3117.004 Million cell updates/sec

Title: US-10-724-532-5

Perfect score: 135
Sequence: 1 gagagaagcctatgcacga.....ccctgcgcgagagagagag 135

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: N_Geneseq_16Dec04:*
2: geneeqn1980a:*
3: geneeqn1990a:*
4: geneeqn2000a:*
5: geneeqn2001a:*
6: geneeqn2002a:*
7: geneeqn2002b:*
8: geneeqn2003a:*
9: geneeqn2003b:*
10: geneeqn2003c:*
11: geneeqn2003d:*
12: geneeqn2004a:*
13: geneeqn2004b:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50.8	37.6	159	3	AAC64967 Pig phosp
2	50.2	37.2	701	10	ADB53082 Primary r
3	46	34.1	159	13	ADR97285
4	46	34.1	306	6	ABN22344
5	46	34.1	480	3	AAC06724 Human ORF
6	46	34.1	525	9	ACH16833 Human sec
7	46	34.1	1635	6	ABL61825
8	46	34.1	1635	12	ADN04087
9	46	34.1	1712	12	ADP21384
10	45	33.3	380	9	ACH16738 Human adu
11	45	33.3	418	9	ACH18023
12	44.4	32.9	394	9	ACH17005 Human adu
13	44.4	32.9	487	9	ACH18165
14	44.2	32.7	312	3	AAZ50498
15	41.2	30.5	407	9	ACH16630 Human adu
16	38	28.1	492	6	ACH30165
17	36.2	26.8	147419	6	ABK83574
18	35	25.9	6481	4	AA159183 Human pol
19	35	25.9	6481	5	ADQ99406 DNA encod
20	35	25.9	6481	9	ADB49166 Novel hum

C 21	35	25.9	6536	3	AAC75801
C 22	35	25.9	10625	5	AAC85836
C 23	35	25.9	10625	6	AA141031
C 24	33.6	24.9	652	6	ABO60653
C 25	33.6	24.9	1896	12	ADP07907
C 26	33.6	24.9	2419	5	ADL62294
C 27	33.6	24.9	2422	10	ADC37617
C 28	33.6	24.9	3647	6	ABK83658
C 29	33.6	24.9	3647	10	ADP81412
C 30	33.6	24.9	3647	13	ADR25399
C 31	33.6	24.9	3647	13	ACN38837
C 32	33.6	24.9	3708	2	AAZ77530
C 33	33.6	24.9	3748	3	AAZ77530
C 34	33.6	24.9	3925	12	ADO21778
C 35	32.6	24.1	113306	10	ADC86554
C 36	31.4	23.3	1938	11	ACN44341
C 37	31.4	23.3	2175	2	AAZ24906
C 38	31.2	23.1	473	13	ADQ79072
C 39	31.2	23.1	2229	6	ABK74380
C 40	30.8	22.8	415	4	AA113308
C 41	30.8	22.8	415	4	ABA55007
C 42	30.8	22.8	415	4	AA134661
C 43	30.8	22.8	415	4	ABA44562
C 44	30.8	22.8	415	4	ABA24770
C 45	30.8	22.8	415	4	AAK28730

ALIGNMENTS

RESULT 1	AAC64967	standard; cDNA; 159 BP.
ID	AAC64967	
XX	XX	
AC	AAC64967;	
XX	XX	
DT	09-FEB-2001 (first entry)	
XX	XX	
DE	Pig phospholamban cDNA.	
XX	XX	
KW	Pig; sarco/endoplasmic reticulum calcium ATPase; SERCA; signalling;	
KW	cardiac hypertrophy; heart failure; hypertension; Darter-White disease;	
KW	Brody's disease; diabetes; ss.	
XX	XX	
OS	Sus scrofa.	
XX	XX	
PN	GB2349217-A.	
XX	XX	
PD	25-OCT-2000.	
XX	XX	
PF	14-APR-2000; 2000GB-00009363.	
XX	XX	
PR	15-APR-1999; 99GB-00008670.	
PR	15-APR-1999; 99US-0129596P.	
PR	01-JUN-1999; 99GB-00012736.	
XX	XX	
PA	(DEWG-) DEWGEN NV.	
XX	XX	
DR	WPI; 2000-658082/64.	
PT	Identifying modulators of sarco/endoplasmic reticulum calcium ATPase.	
PT	useful potentially for treating disorders of calcium homeostasis, e.g.	
PT	cardiac hypertrophy.	
XX	XX	
PS	Disclosure; Fig 11; 108bp; English.	
XX	XX	
CC	The present invention is concerned with methods of using C. elegans to	
CC	identify compounds which are capable of up- and down-regulating the	
CC	activity of the sarco/endoplasmic reticulum calcium ATPase (SERCA). This	
CC	protein is involved in cell signalling, and elevated levels affect	
CC	cellular processes such as contraction, secretion and cell cycling. The	

CC methods can be used to identify compounds for use in the treatment of
CC some muscle pathologies, cardiac hypertrophy, heart failure,
CC hyperension, diabetes, Darier-White disease and Brody's disease
XX

SO Sequence 159 BP; 45 A; 41 C; 22 G; 51 T; 0 U; 0 Other;

Query Match 37.6%; Score 50.8; DB 3; Length 159;
Best Local Similarity 68.6%; Pred. No. 6.9e-06;
Matches 70; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 18 TGAGAGAGGCTCAGGCGCAGACCTCCAGAACTCTTCATGCTTTTGTCTGAT 77
DB 54 TGAATGCTCCACAGACGCTCAAAACCTTCAGAACTTATTCATTTCTGTCTAT 113

OY 78 TCTCATCTGCTCCTGCTGATTTGCAATTGCTATGCTCTCT 119
DB 114 CTTATATGCTCTTCTGCTGATTTGCAATCATCTGATGCTTCT 155

RESULT 2
ID ADB53082 standard; DNA; 701 BP.

XX ADB53082;
AC ADB53082;
XX
DT 04-DEC-2003 (first entry)

DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3624.

XX toxic effect; gene expression profile; hepatotoxicity; diagnostic marker;
KW toxicity marker; toxicity progression; drug screening;
KW primary rat hepatocyte toxicity modelling; gene; ds.

XX Rattus norvegicus.

OS WO2003065993-A2.

PN 14-AUG-2003.

PD 04-FEB-2003; 2003WO-US003482.

XX 04-FEB-2002; 2002US-0353171P.
PR 13-MAR-2002; 2002US-0363534P.
PR 08-APR-2002; 2002US-0370248P.
PR 10-APR-2002; 2002US-0371134P.
PR 10-APR-2002; 2002US-0371135P.
PR 10-APR-2002; 2002US-0371150P.
PR 11-APR-2002; 2002US-0371413P.
PR 19-APR-2002; 2002US-0373601P.
PR 19-APR-2002; 2002US-0373602P.
PR 22-APR-2002; 2002US-0374139P.
PR 08-MAY-2002; 2002US-0378370P.
PR 09-MAY-2002; 2002US-0378652P.
PR 09-MAY-2002; 2002US-0378653P.
PR 09-MAY-2002; 2002US-0378655P.
PR 09-JUL-2002; 2002US-0394230P.
PR 09-JUL-2002; 2002US-0394253P.
PR 04-SEP-2002; 2002US-0407688P.
PR 28-JAN-2003; 2003US-0442900P.

XX (GENE-) GENE LOGIC INC.

PA Mendrick D, Porter M, Johnson K, Higge B, Castle A, Orr M;
PI Elshoff M;

XX WPI; 2003-731472/69.

XX Determining if a compound induces a toxic effect on a tissue or cell, for
PT identifying hepatotoxic compounds, comprises comparing a gene expression
PT profile of a tissue or cell sample to a database of tox mean and non-tox
PT mean values.

XX Claim 44; SEQ ID NO 3624; 874pp; English.

XX The present invention describes a method for determining whether a
CC compound induces a toxic effect on a tissue or cell. The method comprises
CC preparing a gene expression profile of a tissue or cell sample exposed to
CC the compound, and comparing the gene expression profile to a database
CC comprising data or information on the tox mean and non-tox mean value.
CC The method is useful for predicting or identifying at least one toxic
CC effect, particularly hepatotoxicity, of a test or unknown compound. The
CC genes listed in the specification are useful as diagnostic or toxicity
CC markers for the prediction or identification of the physiological state
CC of tissue or cell sample that has been exposed to a compound, or to
CC identify or predict the toxic effects of a compound or an agent. These
CC may also be used as markers for monitoring toxicity progression or for
CC drug screening. The present sequence represents a primary rat hepatocyte
CC toxicity modelling related gene sequence from the present invention.

SO Sequence 701 BP; 184 A; 178 C; 141 G; 198 T; 0 U; 0 Other;

Query Match 37.2%; Score 50.2; DB 10; Length 701;
Best Local Similarity 68.0%; Pred. No. 1.7e-05;
Matches 70; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 18 TGAGAGAGGCTCAGGCGCAGACCTCCAGAACTCTTCATGCTTTTGTCTGAT 77
DB 227 TGAATGCCCCAGAGGCGCTCAAACTTCAGAACTTATTCATTTCTGTCTAT 286

OY 78 TCTCATCTGCTCCTGCTGATTTGCAATTGCTATGCTCTCTG 120
DB 287 CTTGATATGCTCTGCTGATGATCATCATTTGATGCTTCTG 329

RESULT 3
ID ADR97285 standard; DNA; 159 BP.

XX ADR97285;
AC ADR97285;
XX
DT 16-DEC-2004 (first entry)

DE Human phospholamban polymorphism fragment DNA.
KW ds; human; phospholamban; polymorphism; cardiovascular disease.

OS Homo sapiens.

PN US2004191802-A1.

PD 30-SEP-2004.

PF 22-OCT-2003; 2003US-00691412.

PR 22-OCT-2002; 2002US-0420295P.

PA (KRAN/) KRANTAS E G.
PA (HAGH/) HAGHIGHT K.

XX Krantias EG, Haghighi K;

XX WPI; 2004-689841/67.

XX phospholamban polymorphism assessment in individual, for determining risk
PT for developing cardiovascular disease, by comparing analysis of the
PT nucleotide fragment with a predetermined phospholamban nucleotide
PT fragment sequence.

XX Claim 15; SEQ ID NO 1; 15pp; English.

XX The invention relates to a method of phospholamban polymorphism
CC assessment in an individual which comprises comparing the analysis of the
CC nucleotide fragment with a predetermined phospholamban nucleotide
CC fragment sequence to determine whether the individual carries a
CC phospholamban polymorphism. The methods and phospholamban polymorphism
CC fragment are useful for determining if an individual is at risk for

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 7, 2005, 09:02:25 ; Search time 1691.67 Seconds
(without alignments)
3037.641 Million cell updates/sec

Title: US-10-724-532-5
Perfect score: 135
Sequence: 1 gagagaagaactatcatcatga.....tccctgcgcgagagagagag 135

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues
Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: gb_esc1:.*
2: gb_esc2:.*
3: gb_hnc:.*
4: gb_esc3:.*
5: gb_esc4:.*
6: gb_esc5:.*
7: gb_esc6:.*
8: gb_gsa1:.*
9: gb_gsa2:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50.8	37.6	381	5	BX669692 BX669692
2	50.8	37.6	702	5	BX922974 BX922974
3	50.8	37.6	724	5	BX674983 BX674983
4	50.8	37.6	740	5	BX924154 BX924154
5	50.8	37.6	758	5	BX923697 BX923697
6	50.8	37.6	811	7	CK449263 892817 MA
7	50.2	37.2	179	2	BE113353
8	50.2	37.2	377	2	BF547322
9	50.2	37.2	417	1	AI322542
10	50.2	37.2	439	2	BE115006
11	50.2	37.2	449	2	BF394968
12	50.2	37.2	449	2	BE098177
13	50.2	37.2	451	4	BE128891
14	50.2	37.2	454	2	BE099930
15	50.2	37.2	476	2	BF525258
16	50.2	37.2	480	7	CR471116
17	50.2	37.2	487	4	BC379827
18	50.2	37.2	498	1	AI603160
19	50.2	37.2	511	4	BF395370
20	50.2	37.2	513	4	BI296789
21	50.2	37.2	518	2	BE112568
22	50.2	37.2	527	2	BF395607
23	50.2	37.2	528	2	BF395670
24	50.2	37.2	540	2	BF395398

c	25	50.2	37.2	575	4	BI290034	UI-R-DKO-
	26	50.2	37.2	589	2	BF525010	UI-R-ABO-
c	27	50.2	37.2	608	1	AI103929	EST213218
	28	50.2	37.2	699	7	CK358482	AGENCOURT
	29	50.2	37.2	710	7	CK359590	AGENCOURT
	30	50.2	37.2	719	7	CK358464	AGENCOURT
	31	50.2	37.2	719	7	CK356296	AGENCOURT
	32	50.2	37.2	731	7	CK357243	AGENCOURT
	33	50.2	37.2	737	7	CK357232	AGENCOURT
	34	50.2	37.2	737	7	CK355359	AGENCOURT
	35	50.2	37.2	738	7	CK357123	AGENCOURT
	36	50.2	37.2	744	7	CK356439	AGENCOURT
	37	50.2	37.2	744	7	CK357747	AGENCOURT
	38	50.2	37.2	745	7	CK355314	AGENCOURT
	39	50.2	37.2	745	7	CK356371	AGENCOURT
	40	50.2	37.2	748	7	CK359219	AGENCOURT
	41	50.2	37.2	754	7	CK355445	AGENCOURT
	42	50.2	37.2	758	7	CK355453	AGENCOURT
	43	50.2	37.2	758	7	CK357746	AGENCOURT
	44	50.2	37.2	762	7	CK359188	AGENCOURT
	45	50.2	37.2	764	7	CK357447	AGENCOURT

ALIGNMENTS

RESULT 1
BX669692
LOCUS BX669692 381 bp mRNA linear EST 07-MAY-2004
DEFINITION BX669692 Sus scrofa library (scac) Sus scrofa cDNA clone
scac00281.c.02 5prim, mRNA sequence.

ACCESSION BX669692
VERSION BX669692.1 GI:37979481

KEYWORDS
SOURCE

ORGANISM

Sus scrofa (pig)

Sus scrofa

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.

REFERENCE

1 (bases 1 to 381)

Bonner, A., Tosser-Klopp, G., Benne, F., Cabau, C., Villegier, S.,

Soares, M., Bonaldo, F., and Hacey, F.

A Pig Normalised Multi-Tissue cDNA Library

Unpublished (2003)

Contract: Tosser-Klopp G

Genetique Animale

Institut National de la Recherche Agronomique

Chemin de Borde-Rouge - Auzeville BP27, 31326 Castanet-Tolosan

cedex, FRANCE

Tel: 33 (0) 5.61.28.51.14

Fax: 33 (0) 5.61.28.53.08

Email: tosser@toulouse.inra.fr

Sequences cleaned of vector, adaptor and repetitions. Contact us

at sigenast@port@jouy.inra.fr to obtain the Chromatogram of this

sequence.

Plate: 0028 row: c column: 2.

location/Qualifiers

1..381

/organism="Sus scrofa"

/mol_type="mRNA"

/db_xref="taxon:9823"

/clone="scac00281.c.02"

/tissue type="mixed"

/clone_lib="Sus Scrofa library (scac)"

/note="Vector: pT73d-pac vector; tissues: adipose tissue,

brain, kidney, liver, muscle, ovary, testis, heart,

hypothalamus, pancreas, skin, spleen, thymus, placenta,

pituitary gland, seminal vesicle, small intestine,

uterus, adrenals, bulbo urethral gland, cerebral trunk,

epididymis, female gonad, gall-bladder, hippocampus,

large intestine, male gonad, melanocytes, stomach, udder"

Query Match 37.6%; Score 50.8; DB 5; Length 381;

Best Local Similarity 68.6%; Pred. No. 0.00029;
Matches 70; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

```

Oy      18 TGAGAGAAAGGCTCAGGCCAGGCAAGAACCTCAGAAATGCTTTCATTTGTCAT 77
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      82 TGAATGCTCACAAGCAGCAGTCAAAACCTCAGAACTATTATCAATTTGCTCAT 141

```

Oy	78	TCTCATCTGCCTCTCGTCGATTGGCATTAATCGTCATGCTCCT	119
Db	142	CTTAATATATGCGCTCTTGCTGATTTGTCATCGTGATGCTTCT	183

RESULT 2				
LOCUS	BX922974			
DEFINITION	BX922974	702 bp	mRNA	linear
	BX922974	Sus Scrofa library (scan)	Sus scrofa	CDNA clone
	scan0013d.j.14	5prim.	mrna	sequence.
	scan0013d.j.14	5prim.	mrna	sequence.

ACCESSION	BX922974	GI:41139822
VERSION	BX922974.1	
KEYWORDS	EST.	
SOURCE	<i>Sus scrofa</i> (pig)	
ORGANISM	<i>Sus scrofa</i>	

REFERENCE	Eukaryotes: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae.
AUTHORS	1 (bases 1 to 702)
TITLE	Bonne, A., Tosser-Klopp, G., Beme, F., Cabau, C., Villegier, S., Soares, M., Bonaïdo, F. and Haeley, F.
JOURNAL	A Pig Normalised Multi-Tissue cDNA Library
COMMENT	Unpublished (2003)
	Contact: Tosser-Klopp G

Institut National de la Recherche Agronomique
Chemin de Borde-Rouge - Auzeville BP27, 31326 Castanet-Tolosan
cedex, FRANCE
Tel: 33 (0) 5.61.28.51.14
Fax: 33 (0) 5.61.28.53.08
Email: tossner@oulouse.inra.fr
Sequence cleaned of vector, adaptor and repetitions. Contact us
at systemsupport@jouy.inra.fr to obtain the chromatogram of this
sequence.
Plate: 0013 row: j column: 14.

FEATURES	Location/Qualifiers
source	1. .702

```

/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9623"
/clone="scan0013d.j.14"
/tissue_type="mixed"
/dev stage="from embryos to adults"
/clone_id="Sus scrofa library (scan)"
/note="tissues: adipose tissue, brain, kidney, liver,
muscle, ovary, testis, heart, hypothalamus, pancreas,
skin, spleen, thymus, placenta, pituitary gland, seminal
vesicle, small intestine, uterus, adrenals, bulbo urethral
gland, cerebral trunk, epididymis, female gonad,
gall-bladder, hippocampus, large intestine, male gonad,
melanocytes, stomach, udder"

```

ORIGIN

Query Match	37.6%	Score 50.8;	DB 5;	Length 702;
Best Local Similarity	68.6%	Pred. No. 0.00033;		
Matches 70; Conservative	0;	Mismatches 32;	Indels 0;	Gaps 0

Oy 18 TGAGGAAAGCCCTCAGGCCACGGCAGAACCCTCGAAGATGCTTTCATTGTCTCAT 77
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 216 TGAATGCCTCAACAAGCACGTCAAAACCTTGAGACCTATTATTCATTTCTGCTCAT 275

Qy	78	TCTCATCTGCCCTCCCTGCTGATTTGCATTATCGTACGCTCT	115
Db	276	CTTAATATGCGCTCTTGCTGATTTGCATCATCGTGATGCTTCT	317

RESULT 3

EX674983	724 bp	mRNA	linear	EST 07-MAY-2004
LOCUS	EX674983	Sus Scrofa library (scac)	Sus scrofa cDNA clone	
DEFINITION	scac00391.h.23 5prim,	mRNA sequence.		

ACCESSION	EX674983
VERSION	EX674983.1
KEYWORDS	GI:38008935 EST.

SOURCE	Sus scrofa (pig)
ORGANISM	Sus scrofa

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE
AUTHORS
1 (bases 1 to 724)
Bonnet, A., Tossier-Klopp, G., Benne, F., Cabau, C., Villegier, S.,
Scares, M., Ronaldo, F. and Hafev, F.

TITLE	A Pig Normalised Multi-Tissue cDNA Library
JOURNAL	Unpublished (2003)

COMMENT

Institut National de la Recherche Agronomique
Chemin de Borde-Rouge - Auzeville BP27, 31326 Castanet-Tolosan
cedex, FRANCE

Tel: 33 (0) 5.61.28.51.14
Fax: 33 (0) 5.61.28.53.08
Email: rosier@coulouze.inra.fr
Sequence cleaned of vector, adaptor and repetitions. Contact us at s4gensupport@jouy.inra.fr to obtain the chromatogram of this sequence.
Plate: 0039, row: h column: 23.

FEATURES	Location/Qualifiers
source	1. .724

```

/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="scac00391.h.23"
/tissue_type="mixed"
/clone_lib="Sus Scrofa library (scac)"
/note="Vector: p773D-pb vector; tissues: adipose tissue,
brain, kidney, liver, muscle, ovary, testis, heart,
hypothalamus, pancreas, skin, spleen, thymus, placenta,
pituitary gland, seminal vesicle, small intestine,
uterus, adrenals, bulbo urethral gland, cerebral trunk,
epididymus, female gonad, gall-bladder, hippocampus,
large intestine, male gonad, melanocytes, stomach, udder"

```

ORIGIN

Query Match	37.6%	Score 50.8	DB 5	Length 724
Best Local Similarity	68.6%	Pred. No. 0.00033		
Matches 70; Conservative	0;	Mismatches 32;	Indels 0;	Gaps 0;

```

Oy      18  TGAGGAGAGGCGCTCAGGCCAGGCGAGAACCTCCAGAAATGCTTCATGCTTTTGTCTGAT  77
          |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      237  TGAATATGCTTCACAGACGCTCAAAACCTTCAGAACCTAATTATCATATTCTGTCTCAT  296

```

```

OY      78 TCTCATCTGCCTCCTGCTGATTTCATTTGCATTATCGTCAAGTCTCT 119
          ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     297 CTTAATATGCCCTCTTGCTGATTTCATTCATCATCGTAGTCTTCT 338

```

RESULT 4

LOCUS	740 bp	MRNA	linear	EST 07-MAY-2004
DEFINITION	BX924154	Sus Scrofa library (scan)	Sus scrofa CDNA clone	
	BX924154	Sus Scrofa library (scan)	Sus scrofa CDNA clone	
	scan001d.f.23	5prim.	mrna sequence.	

ACCESSION	EX924154
VERSION	EX924154.1
	GI:41141002

KEYWORDS	EST.
SOURCE	Sus scrofa (pig)
ORIGIN	...

ORGANISM
Sus scrofa
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.

REFERENCE
AUTHORS
1 (bases 1 to 740)
Bonnet, A., Tosser-Klopp, G., Benne, F., Cabau, C., Villegier, S.,
Soares, M., Bonaldo, F. and Hately, F.

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 7, 2005, 09:02:25 ; Search time 77.2222 Seconds
(without alignments)
2860.541 Million cell updates/sec

Title: US-10-724-532-5

Perfect score: 135

Sequence: 1 gagagaagcctatgcacga.....tccgtcgcgagagagag 135

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PTCDS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50.8	37.6	159	US-09-549-872B-9	Sequence 9, Appl
2	50.8	37.6	159	US-09-549-872B-13	Sequence 13, Appl
3	46	34.1	1480	US-09-513-999C-10799	Sequence 10799, A
4	46	34.1	1635	US-09-949-016-1439	Sequence 1439, Ap
5	46	34.1	16062	US-09-949-016-13181	Sequence 13181, A
6	44.2	32.7	315	US-09-124-671-26	Sequence 26, Appl
7	35	25.3	6481	US-09-620-312D-1076	Sequence 1076, Ap
8	31.4	22.3	1917	US-08-914-999-3	Sequence 3, Appl
9	30.6	22.7	1917	US-09-902-540-3588	Sequence 3588, Ap
10	30.6	22.7	19394	US-09-902-540-1172	Sequence 1172, Ap
11	30.2	22.4	65424	US-09-949-016-12426	Sequence 12426, A
12	30.2	22.4	74353	US-09-949-016-15336	Sequence 15336, A
13	29.6	21.9	957	US-08-309-182B-1	Sequence 1, Appl
14	29.6	21.9	8590	US-09-949-016-5562	Sequence 5562, Ap
15	29.6	21.9	10300	US-09-949-016-636	Sequence 636, App
16	29.6	21.9	38575	US-09-949-016-12378	Sequence 12378, A
17	29.6	21.9	11915	US-09-949-016-12378	Sequence 12378, A
18	29.2	21.6	1095	US-09-252-991A-14880	Sequence 14880, A
19	29.2	21.6	1317	US-09-252-991A-14748	Sequence 14748, A
20	29.2	21.6	2622	US-09-252-991A-15001	Sequence 15001, A
21	29	21.5	474	US-09-513-999C-1161	Sequence 1161, Ap
22	29	21.5	601	US-09-949-016-202802	Sequence 202802,
23	29	21.5	1123	US-09-188-930-28	Sequence 28, Appl
24	29	21.5	1123	US-09-188-930-203	Sequence 203, Appl
25	29	21.5	1123	US-09-312-283C-28	Sequence 28, Appl
26	29	21.5	1123	US-09-312-283C-203	Sequence 203, App
27	29	21.5	26050	US-09-949-016-17449	Sequence 17449, A

28	28.8	21.3	879	US-09-489-039A-5041	Sequence 5041, Ap
29	28.6	21.2	601	US-09-949-016-200644	Sequence 200644,
30	28.6	21.2	601	US-09-949-016-200790	Sequence 200790,
31	28.6	21.2	46343	US-09-949-016-16824	Sequence 16824, A
32	28.6	21.2	152582	US-09-949-016-12086	Sequence 12086, A
33	28.6	21.2	152583	US-09-949-016-17390	Sequence 17390, A
34	28.6	21.2	152583	US-09-949-016-17391	Sequence 17391, A
35	28.6	21.2	1664976	US-08-916-421B-1	Sequence 1, Appl
36	28.6	21.2	1664976	US-09-692-570-1	Sequence 1, Appl
37	28.4	21.0	1855	US-09-949-016-1929	Sequence 1929, Ap
38	28.4	21.0	162914	US-09-949-016-15578	Sequence 15578, A
39	28.2	20.9	568	US-08-956-171E-999	Sequence 999, App
40	28.2	20.9	568	US-08-781-986A-999	Sequence 999, App
41	28.2	20.9	603	US-08-816-346-5	Sequence 5, Appl
42	28.2	20.9	603	US-09-335-411-5	Sequence 5, Appl
43	28.2	20.9	1851	US-09-949-016-3036	Sequence 3036, Ap
44	28.2	20.9	2120	US-09-149-476-160	Sequence 160, App
45	28.2	20.9	2907	US-08-816-346-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-09-549-872B-9
; Sequence 9, Application US/09549872B
; Patent No. 6540996
; GENERAL INFORMATION:
; APPLICANT: Zwaal, Richard
; APPLICANT: Groenen, Jose
; APPLICANT: Bogaert, Thierry
; TITLE OF INVENTION: COMPOUND SCREENING METHODS
; FILE REFERENCE: D00590/70008 (JRV/RE)
; CURRENT APPLICATION NUMBER: US/09/549,872B
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: GB 9908670.4
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: US 60/129,596
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: GB 9912736.7
; PRIOR FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 159
; TYPE: DNA
; ORGANISM: Sus sp.
US-09-549-872B-9

Query Match
Best Local Similarity 37.6%; Score 50.8; DB 4; Length 159;
Matches 70; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 18 TGAGGAAGGCTCAGGCGAGACCTCCAGATGCTTCATTTGCTGAT 77
DB 54 TGAATGCTCAAGACGACGCTCAACCTTGAACCATTTGCTGAT 113
QY 78 TCTATGCTCCTCTGCTGATTTGATATGCTATGCTCT 119
DB 114 CTTATATGCTCCTCTGCTGATTTGATATGCTATGCTCT 155

RESULT 2
US-09-549-872B-13
; Sequence 13, Application US/09549872B
; Patent No. 6540996
; GENERAL INFORMATION:
; APPLICANT: Zwaal, Richard
; APPLICANT: Groenen, Jose
; APPLICANT: Bogaert, Thierry
; TITLE OF INVENTION: COMPOUND SCREENING METHODS
; FILE REFERENCE: D00590/70008 (JRV/RE)
; CURRENT APPLICATION NUMBER: US/09/549,872B

;; CURRENT FILING DATE: 2000-04-14
;; PRIOR APPLICATION NUMBER: GB 9908670.4
;; PRIOR FILING DATE: 1999-04-15
;; PRIOR APPLICATION NUMBER: US 60/129,596
;; PRIOR FILING DATE: 1999-04-15
;; PRIOR APPLICATION NUMBER: GB 9912736.7
;; PRIOR FILING DATE: 1999-06-01
;; NUMBER OF SEQ ID NOS: 39
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 13
;; LENGTH: 159
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: HUMANIZED PIG
;; OTHER INFORMATION: PUB CDNA
US-09-549-872B-13

Query Match 37.6%; Score 50.8; DB 4; Length 159;
Best Local Similarity 68.6%; Pred. No. 1.2e-07;
Matches 70; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 18 TGAAGAGGCTCAGGCGCAGACCTCCAGAACTCTTCATGCTTTTGTGTCAT 77
DB 54 TGAATGCTTCACAGCAGCCTCAAAACCTTCAGAACTTATTCATTTCTGTCTCAT 113
QY 78 TCTCATCTGCTCCTGCTGATTTGATTCATTCATGCTCTCT 119
DB 114 CTTAATATGCTCTTCTGCTGATTTGATTCATTCATGCTCTCT 155

RESULT 3
US-09-513-999C-10799
;; Sequence 10799, Application US/09513999C
;; Patent No. 6783961
;; GENERAL INFORMATION:
;; APPLICANT: Dumas Milne Edwards, J.B.
;; APPLICANT: Duclet, A.
;; APPLICANT: Giorlando, J.Y.
;; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
;; FILE REFERENCE: 59, US2, REG
;; CURRENT APPLICATION NUMBER: US/09/513,999C
;; CURRENT FILING DATE: 2000-02-24
;; PRIOR APPLICATION NUMBER: US 60/122,487
;; PRIOR FILING DATE: 1999-02-26
;; NUMBER OF SEQ ID NOS: 36681
;; SOFTWARE: Patent.pm
;; SEQ ID NO 10799
;; LENGTH: 480
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-513-999C-10799

Query Match 34.1%; Score 46; DB 4; Length 480;
Best Local Similarity 65.7%; Pred. No. 8.4e-06;
Matches 67; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 18 TGAAGAGGCTCAGGCGCAGACCTCCAGAACTCTTCATGCTTTTGTGTCAT 77
DB 249 TGAATGCTTCACAGCAGCCTCAAAAGCTACAGAACTTATTCATTTCTGTCTCAT 308
QY 78 TCTCATCTGCTCCTGCTGATTTGATTCATTCATGCTCTCT 119
DB 309 CTTAATATGCTCTTCTGCTGATTCATTCATGCTCTCT 350

RESULT 4
US-09-949-016-1439
;; Sequence 1439, Application US/09949016
;; Patent No. 6812339
;; GENERAL INFORMATION:
;; APPLICANT: VENTER, J. Craig et al.

;; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;; FILE REFERENCE: CLO01307
;; CURRENT APPLICATION NUMBER: US/09/949,016
;; CURRENT FILING DATE: 2000-04-14
;; PRIOR APPLICATION NUMBER: 60/241,755
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/237,768
;; PRIOR FILING DATE: 2000-10-03
;; PRIOR APPLICATION NUMBER: 60/231,498
;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 207012
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 1439
;; LENGTH: 1635
;; TYPE: DNA
;; ORGANISM: Human
US-09-949-016-1439

Query Match 34.1%; Score 46; DB 4; Length 1635;
Best Local Similarity 65.7%; Pred. No. 1.5e-05;
Matches 67; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 18 TGAAGAGGCTCAGGCGCAGACCTCCAGAACTCTTCATGCTTTTGTGTCAT 77
DB 235 TGAATGCTTCACAGCAGCCTCAAAAGCTACAGAACTTATTCATTTCTGTCTCAT 294
QY 78 TCTCATCTGCTCCTGCTGATTTGATTCATTCATGCTCTCT 119
DB 295 CTTAATATGCTCTTCTGCTGATTCATTCATGCTCTCT 336

RESULT 5
US-09-949-016-13181
;; Sequence 13181, Application US/09949016
;; Patent No. 6812339
;; GENERAL INFORMATION:
;; APPLICANT: VENTER, J. Craig et al.
;; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;; FILE REFERENCE: CLO01307
;; CURRENT APPLICATION NUMBER: US/09/949,016
;; CURRENT FILING DATE: 2000-04-14
;; PRIOR APPLICATION NUMBER: 60/241,755
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/237,768
;; PRIOR FILING DATE: 2000-10-03
;; PRIOR APPLICATION NUMBER: 60/231,498
;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 207012
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 13181
;; LENGTH: 16062
;; TYPE: DNA
;; ORGANISM: Human
US-09-949-016-13181

Query Match 34.1%; Score 46; DB 4; Length 16062;
Best Local Similarity 65.7%; Pred. No. 4.2e-05;
Matches 67; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 18 TGAAGAGGCTCAGGCGCAGACCTCCAGAACTCTTCATGCTTTTGTGTCAT 77
DB 12661 TGAATGCTTCACAGCAGCCTCAAAAGCTACAGAACTTATTCATTTCTGTCTCAT 12720
QY 78 TCTCATCTGCTCCTGCTGATTTGATTCATTCATGCTCTCT 119
DB 12721 CTTAATATGCTCTTCTGCTGATTCATTCATGCTCTCT 12762

RESULT 6
US-09-124-671-26
;; Sequence 26, Application US/09124671A

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Comphen Ltd.

OM nucleic - nucleic search, using BW model

Run on: July 7, 2005, 09:22:55 ; Search time 325.556 Seconds
(without alignments)
2603.465 Million cell updates/sec

Title: US-10-724-532-5

Perfect score: 135
Sequence: 1 gagagaagcctatgcacga.....tcctgcgcagagagagag 135

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 6330943 seqs, 3139157217 residues

Total number of hits satisfying chosen parameters: 12661886

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA.*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US05_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
15: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
16: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
17: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
18: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
19: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
20: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
21: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
22: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
23: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	135	100.0	135	20	US-10-724-532-5
2	135	100.0	135	20	US-10-724-532-5
3	108	80.0	108	20	US-10-724-532-3
4	108	80.0	108	20	US-10-724-532-4
5	50.8	37.6	159	15	US-10-371-101-9
6	50.8	37.6	159	15	US-10-371-101-13
7	46	34.1	159	19	US-10-691-412-1

8	46	34.1	525	10	US-09-918-995-4045	Sequence 4045, Ap
9	46	34.1	1635	10	US-09-873-367C-162	Sequence 162, App
10	46	34.1	1635	21	US-10-843-641A-162	Sequence 162, App
11	45	33.3	3950	10	US-09-918-995-3950	Sequence 3950, Ap
12	45	33.3	418	10	US-09-918-995-5235	Sequence 5235, Ap
13	44.4	32.9	394	10	US-09-918-995-4217	Sequence 4217, Ap
14	44.4	32.9	487	10	US-09-918-995-5377	Sequence 5377, Ap
15	44.2	32.7	315	20	US-10-815-514-26	Sequence 26, Appl
16	44.2	32.7	315	20	US-10-877-910-26	Sequence 26, Appl
17	44.2	32.7	315	21	US-10-873-554-26	Sequence 26, Appl
18	41.2	30.5	407	10	US-09-918-995-3842	Sequence 3842, Ap
19	38	28.1	492	10	US-09-918-995-17377	Sequence 17377, A
20	35	25.9	6481	15	US-10-037-270-1076	Sequence 1076, Ap
21	35	25.9	6481	17	US-10-117-722-1076	Sequence 1076, Ap
22	35	25.9	10625	9	US-09-727-384-5	Sequence 5, Appl
23	35	25.9	10625	14	US-10-023-219-3	Sequence 3, Appl
24	35	25.9	10625	21	US-10-650-276-3	Sequence 3, Appl
25	33.6	24.9	652	11	US-09-969-034-4348	Sequence 4348, Ap
26	33.6	24.9	1896	21	US-10-723-518-2	Sequence 2, Appl
27	33.6	24.9	2180	18	US-10-425-114-557	Sequence 557, App
28	33.6	24.9	2220	20	US-10-425-115-167740	Sequence 167740, A
29	33.6	24.9	2419	10	US-09-814-353-20506	Sequence 20506, A
30	33.6	24.9	3647	17	US-10-172-118-1260	Sequence 1260, Ap
31	33.6	24.9	3647	18	US-10-342-857-1260	Sequence 1260, Ap
32	33.6	24.9	3647	21	US-10-848-755A-148	Sequence 148, App
33	33.6	24.9	3748	9	US-09-925-301-80	Sequence 80, Appl
34	33.6	24.9	3925	20	US-10-723-860-4598	Sequence 4598, Ap
35	32.6	24.1	113306	17	US-10-292-798-1007	Sequence 1007, Ap
36	32.2	22.9	613	19	US-10-767-701-25701	Sequence 25701, A
37	31.4	23.3	1938	13	US-10-087-192-740	Sequence 740, App
38	31.4	23.3	2175	9	US-09-994-485-7	Sequence 7, Appl
39	31.4	23.3	2175	9	US-09-832-292-7	Sequence 8641, A
40	31.2	23.1	1137	19	US-10-437-963-86841	Sequence 1671, Ap
41	31.2	23.1	2229	9	US-09-974-300-1671	Sequence 3236, Ap
42	30.8	22.8	415	9	US-09-864-761-3236	Sequence 78016, A
43	30.6	22.7	639	21	US-10-470-048B-40	Sequence 43089, A
44	30.6	22.7	1591	19	US-10-437-963-78016	
45	30.6	22.7	1878	17	US-10-369-493-43089	

ALIGNMENTS

RESULT 1
US-10-724-532-5
; Sequence 5, Application US/10724532
; Publication No. US20040203027A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Thomas D
; TITLE OF INVENTION: Signal for Targeting Molecules to the Sarco(endo)plasmic
; FILE REFERENCE: SR RPA
; CURRENT APPLICATION NUMBER: US/10/724, 532
; PRIOR FILING DATE: 2003-11-29
; PRIOR APPLICATION NUMBER: US 60/430322
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 135
; TYPE: DNA
; ORGANISM: mus musculus
US-10-724-532-5

Query Match 100.0%; Score 135; DB 20; Length 135;
Best Local Similarity 100.0%; Pred. No. 7; 7e-36;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGAGAAAGCTTATGCATGAGAGAAAGGCTCAGGCGAGAAAGCTTCAGAAAGCTTTC 60
DB 1 GAGAGAAAGCTTATGCATGAGAGAAAGGCTCAGGCGAGAAAGCTTCAGAAAGCTTTC 60
QY 61 ATTGCTTTTGTGATTCATCTCATCTGCTCTGCTGATTCATATGATGATGCTCTCTG 120

Query Match	37.6%;	Score 50.8;	DB 15;	Length 159;
Best Local Similarity	68.6%;	Pred. No. 4.2e-07;		
Matches 70; Conservative		0; Mismatches 32;	Indels 0;	Gaps 0

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 7, 2005, 09:02:25 ; Search time 1249.17 Seconds
(without alignments)
5236.654 Million cell updates/sec

Title: US-10-724-532-6
Perfect score: 135
Sequence: 1 ctcctctctcgcagcagga.....tcacgcatcagcttctctc 135

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues
Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pal:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_ets:*
12: gb_ey:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52.4	38.8	858	4	RABPHLAM2
2	52.4	38.8	2841	4	OCPHLAM
3	50.8	37.6	159	6	BD247907
4	50.8	37.6	159	6	BD247911
5	50.8	37.6	159	6	AR302003
6	50.8	37.6	159	6	AR302007
7	50.8	37.6	159	6	AX040487
8	50.8	37.6	159	6	AX040491
9	50.8	37.6	737	4	SSFLB
10	50.2	37.2	159	10	S95853
11	50.2	37.2	386	10	S95849
12	50.2	37.2	701	10	RNPPLAMB
13	50.2	37.2	1786	10	RATPHOLA02
14	50.2	37.2	223728	2	AC097906
15	50.2	37.2	231910	2	AC128365
16	47.6	35.3	130240	5	BX276081
17	47.4	35.1	133901	5	BX537355
18	47	34.8	648	10	BC061097
19	47	34.8	940	10	S46792

20	47	34.8	79895	2	AC100317	Mus muscu
21	47	34.8	177018	2	AC099716	Mus muscu
22	46.6	34.5	3312	5	CHKPLB	Chicken car
23	46.6	34.5	3423	5	CHKPLB2	Chicken pho
24	46	34.1	306	6	CQ447405	Sequence
25	46	34.1	323	9	HDMPLAM	Human phosph
26	46	34.1	480	6	AX894936	Sequence
27	46	34.1	480	6	BD030469	Sequence
28	46	34.1	980	9	HSP18G2	AF177764 Homo sap1
29	46	34.1	1635	6	CQ718671	Homo sap1
30	46	34.1	1635	6	AX329653	Sequence
31	46	34.1	1635	9	HDMPLAM	Human phosph
32	46	34.1	1691	9	BC005269	Homo sap1
33	46	34.1	60797	2	AL355356	Homo sap1
34	46	34.1	66092	2	AL136974	Homo sap1
35	46	34.1	150290	9	HS0914	Human DNA
36	44.4	32.9	314	4	AY514751	Canis fam
37	44.4	32.9	832	4	DOGPHL	Canine card
38	44.4	32.9	832	4	DOGPLBA	Dog card
39	44.4	32.9	2614	4	CPPLX	Dog phospho
40	44.2	32.7	315	6	AR121629	Sequence
41	36.2	26.8	147419	9	HS338P11	Human DNA
42	35.6	26.4	184450	2	AC116417	Mus muscu
43	35.2	26.1	209299	5	AC145916	Gallus ga
44	35	25.9	5702	6	CQ719769	Sequence
45	35	25.9	6481	6	AR339585	Sequence

ALIGNMENTS

RESULT 1	RABPHLAM2	858 bp	DNA	linear	MM 27-APR-1993
LOCUS	RABPHLAM2				
DEFINITION	Rabbit phospholamban gene, partial exon 2.				
ACCESSION	M63601				
VERSION	M63601.1 GI:165636				
KEYWORDS	phospholamban.				
SEGMENTS	2 of 3				
SOURCE	Oryctolagus cuniculus (rabbit)				
ORGANISM	Oryctolagus cuniculus				
REFERENCE	Bukacynska, Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus. Fujii, J., Zarain-Herzberg, A., Willard, H. F., Tada, M. and MacLennan, D. H. Structure of the rabbit phospholamban gene, cloning of the human cDNA, and assignment of the gene to human chromosome 6 (bases 1 to 858)				
AUTHORS	Fujii, J., Zarain-Herzberg, A., Willard, H. F., Tada, M. and MacLennan, D. H.				
TITLE	Structure of the rabbit phospholamban gene, cloning of the human cDNA, and assignment of the gene to human chromosome 6				
JOURNAL	J. Biol. Chem. 266 (18), 11669-11675 (1991)				
MEDLINE	91268032				
PUBMED	1828805				
COMMENT	Original				
FEATURES	source text: Rabbit DNA. Location/Qualifiers				
source	1..858				
	/organism="Oryctolagus cuniculus"				
	/mol_type="genomic DNA"				
	/db_xref="taxon:9986"				
	/tissue_id="rabbit genomic"				
	join(M63600.1:855..943,428..858)				
exon	/product="phospholamban"				
	428..858				
	/product="phospholamban"				
	/number=2				
CDS	524..682				
	/function="regulatory protein of sarcoplasmic reticulum Ca-ATPase"				
	/codon_start=1				
	/product="phospholamban"				
	/protein_id="AA31445.1"				
	/db_xref="GI:165639"				
	/translation="MEKQVLTGSAIRRASTIEMPOARQNLQNLFINPCLILCLLL ICIIVMLL"				
ORIGIN					

Query Match 38.8%; Score 52.4; DB 4; Length 858;
Best Local Similarity 69.6%; Pred. No. 1.1e-05;
Matches 71; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

Qy 17 AGAGCATGAGCATTAATGCAATTCAGCAGAGCGCATGAGATCAGACAAAAGCAATG 76
|||
Db 678 AGAAGCATGAGCATATGATGATCAGCAGAGACATATCAAGATGACAGAAATTGATA 619
|||

Qy 77 AAAGCATCTGGAGGTTCTGCTGCGCTGAGCGCTTCTCTCA 118
|||
Db 618 AATAGCTTCTGGAGGTTTGAAGCTGCTGTTGAGGCATTTC 577
|||

RESULT 2
OCPHAM/c
LOCUS OCPHAM 2841 bp mRNA linear MAM 24-JUL-1992
DEFINITION O.cuniculus mRNA for phospholamban.
ACCESSION Y00761
VERSION Y00761.1 GI:11661
KEYWORDS phospholamban.
SOURCE Oryctolagus cuniculus (rabbit)
ORGANISM Oryctolagus cuniculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
REFERENCE 1 (bases 1 to 2841)
AUTHORS Fujii,J., Lytton,J., Tada,M. and MacLennan,D.H.
TITLE Rabbit cardiac and slow-twitch muscle express the same
JOURNAL PNAS Lett. 227 (1), 51-55 (1988)
MEDLINE 88112222
PUBMED 2962883

FEATURES
source location/Qualifiers
1..2841
/organism="Oryctolagus cuniculus"
/mol_type="mRNA"
/db_xref="taxon:9986"
178..336
/codon_start=1
/product="phospholamban"
/protein_id="CA68730.1"
/db_xref="GI:1662"
/db_xref="GOA:P20006"
/db_xref="UniProt/Swiss-Prot:P20006"
/translation="MEKTVYLTRSAIRASTIEMPOQARONLQNLFINFCLILCLL
ICIIIVML"

ORIGIN
Query Match 38.8%; Score 52.4; DB 4; Length 2841;
Best Local Similarity 69.6%; Pred. No. 1.3e-05;
Matches 71; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

Qy 17 AGAGCATGAGCATTAATGCAATTCAGCAGAGCGCATGAGATCAGACAAAAGCAATG 76
|||
Db 332 AGAAGCATGAGCATATGATGATCAGCAGAGACATATCAAGATGACAGAAATTGATA 273
|||

Qy 77 AAAGCATCTGGAGGTTCTGCTGCGCTGAGCGCTTCTCTCA 118
|||
Db 272 AATAGCTTCTGGAGGTTTGAAGCTGCTGTTGAGGCATTTC 231
|||

RESULT 3
BD247907/c
LOCUS BD247907 159 bp DNA linear PAT 17-JUL-2003
DEFINITION Method for screening compounds.
ACCESSION BD247907
VERSION BD247907.1 GI:33057677
KEYWORDS JP 2002541859-A/9.
SOURCE Sus sp.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 159)

AUTHORS Zwaal,R., Groenen,J. and Bogaert,T.
TITLE Method for screening compounds
JOURNAL Patent: JP 2002541859-A 9 10-DEC-2002;
DEVGEN NV

COMMENT
OS Sus sp. (pig)
PN JP 2002541859-A/9
PD 10-DEC-2002
PF 14-APR-2000 JP 2000612503
PR 15-APR-1999 GB 9908670.4,15-APR-1999 US 60/129596 PR
01-JUN-1999 GB 9912736.7
PI RICHARD ZWAAL,JOSE GROENEN,THIERRY BOGAERT
PC C12Q1/42,C12N15/09,C12Q1/02,C12N15/00
CC Method for screening compounds
FH Key Location/Qualifiers
FT source 1..159
/organism="Sus sp. (pig)".
location/Qualifiers
1..159
/organism="Sus sp."
/mol_type="genomic DNA"
/db_xref="taxon:9826"

ORIGIN
Query Match 37.6%; Score 50.8; DB 6; Length 159;
Best Local Similarity 68.6%; Pred. No. 3.1e-05;
Matches 70; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

Qy 17 AGAGCATGAGCATTAATGCAATTCAGCAGAGCGCATGAGATCAGACAAAAGCAATG 76
|||
Db 155 AGAAGCATGAGCATATGATGATCAGCAGAGCGCATTAAGATGACAGAAATTGATA 96
|||

Qy 77 AAAGCATCTGGAGGTTCTGCTGCGCTGAGCGCTTCTCTCA 118
|||
Db 95 AATAGCTTCTGAAGGTTTGAAGCTGCTGTTGAGGCATTTC 54
|||

RESULT 4
BD247911/c
LOCUS BD247911 159 bp DNA linear PAT 17-JUL-2003
DEFINITION Method for screening compounds.
ACCESSION BD247911
VERSION BD247911.1 GI:33057681
KEYWORDS JP 2002541859-A/13.
SOURCE Sus sp.
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 159)
AUTHORS Zwaal,R., Groenen,J. and Bogaert,T.
TITLE Method for screening compounds
JOURNAL Patent: JP 2002541859-A 13 10-DEC-2002;
DEVGEN NV

COMMENT
OS Artificial Sequence
PN JP 2002541859-A/13
PD 10-DEC-2002
PF 14-APR-2000 JP 2000612503
PR 15-APR-1999 GB 9908670.4,15-APR-1999 US 60/129596 PR
01-JUN-1999 GB 9912736.7
PI RICHARD ZWAAL,JOSE GROENEN,THIERRY BOGAERT
PC C12Q1/42,C12N15/09,C12Q1/02,C12N15/00
CC Description of Artificial Sequence: HUMANIZED PIG PLB CDNA FH
FH Key Location/Qualifiers
FT source 1..159
/organism="Artificial Sequence".
location/Qualifiers
1..159
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 37.6%; Score 50.8; DB 6; Length 159;
Best Local Similarity 68.6%; Pred. No. 3.1e-05;
Matches 70; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 7, 2005, 09:02:25 ; Search time 256.389 Seconds
(without alignments)
317.004 Million cell updates/sec

Title: US-10-724-532-6

Perfect score: 135
Sequence: 1 cctctctctctcgagcagga.....tcattgataagcttctctc 135

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 10%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001s:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES.

Result No.	Score	Query Match	Length	DB ID	Description
C 1	50.8	37.6	159	3 AAC64967	AAC64967 Pig phosp
C 2	50.2	37.2	701	10 ADB53082	ADB53082 Primary r
C 3	46	34.1	159	13 ADR97285	ADR97285 Human rho
C 4	46	34.1	306	6 ABR22344	ABR22344 Human ORF
C 5	46	34.1	480	9 AAC06724	AAC06724 Human sec
C 6	46	34.1	525	9 ACH16833	ACH16833 Human adu
C 7	46	34.1	1635	6 ABL61825	ABL61825 Colon ade
C 8	46	34.1	1635	12 ADR04087	ADR04087 Antlpsort
C 9	46	34.1	1712	12 ADR21384	ADR21384 Gene PLN
C 10	45	33.3	380	9 ACH16738	ACH16738 Human adu
C 11	45	33.3	418	9 ACH18073	ACH18073 Human adu
C 12	44.4	32.9	394	9 ACH17005	ACH17005 Human adu
C 13	44.4	32.9	487	9 ACH18165	ACH18165 Human adu
C 14	44.2	32.7	312	3 AAZ50498	AAZ50498 KDEL rece
C 15	41.2	30.5	407	9 ACH16630	ACH16630 Human adu
C 16	38	28.1	492	9 ACH30165	ACH30165 Human tes
C 17	36.2	26.8	147419	6 ABR83574	ABR83574 Human CDN
C 18	35	25.9	6481	4 AA159183	AA159183 Human pol
C 19	35	25.9	6481	5 ADO99406	ADO99406 DNA encod
C 20	35	25.9	6481	9 ADB49166	ADB49166 Novel hum

21	35	25.9	6536	3 AAC75801	AAC75801 Human ORF
22	35	25.9	10625	5 AAC85836	AAC85836 Nucleotid
23	35	25.9	10625	6 AA141031	AA141031 DNA encod
24	33.6	24.9	652	6 ABO60553	ABO60553 Human col
25	33.6	24.9	1896	12 ADP07807	ADP07807 Human RAD
26	33.6	24.9	2419	5 ADP62294	ADP62294 Human ova
27	33.6	24.9	2422	10 ADC37617	ADC37617 Human nuc
28	33.6	24.9	3647	6 ABR83658	ABR83658 Human CDN
29	33.6	24.9	3647	10 ADF81412	ADF81412 Leukaemia
30	33.6	24.9	3647	13 ADR25399	ADR25399 Breast ca
31	33.6	24.9	3647	13 ACR38837	ACR38837 Tumour-as
32	33.6	24.9	3708	2 AAZ77530	AAZ77530 Human ova
33	33.6	24.9	3748	3 AAC77686	AAC77686 Human can
34	33.6	24.9	3925	12 ADQ21778	ADQ21778 Human bof
35	32.6	24.1	113306	10 ADC86554	ADC86554 Human GPC
C 36	31.4	23.3	1938	11 ACN44341	ACN44341 Mouse mRN
37	31.4	23.3	2175	2 AAX24906	AAX24906 Mouse elo
38	31.2	23.1	473	13 ADQ79072	ADQ79072 Novel can
39	31.2	23.1	2229	6 ABR74380	ABR74380 Bacillus
40	30.8	22.8	415	4 AA113308	AA113308 Probe #32
41	30.8	22.8	415	4 ABA55007	ABA55007 Human foe
42	30.8	22.8	415	4 AA134661	AA134661 Probe #33
43	30.8	22.8	415	4 ABA44562	ABA44562 Human bte
44	30.8	22.8	415	4 ABA24770	ABA24770 Probe #32
45	30.8	22.8	415	4 AAX28730	AAX28730 Human bon

ALIGNMENTS

RESULT 1
AAC64967/c
ID AAC64967 strand: cDNA; 159 BP.
XX
AC AAC64967;
XX
DT 09-FEB-2001 (first entry)
XX
XX Pig phospholamban cDNA.
DE
XX
XX Pig, sarco/endoplasmic reticulum calcium ATPase; SERCA; signalling;
KW cardiac hypertrophy; heart failure; hypertension; Daxier-White disease;
KW Brody's disease; diabetes; ss.
XX
XX
OS Sus scrofa.
XX
XX GB2349217-A.
XX
XX
PD 25-OCT-2000.
XX
XX
PF 14-APR-2000; 2000GB-00009361.
XX
XX
PR 15-APR-1999; 99GB-00008670.
PR 15-APR-1999; 99US-0129596P.
PR 01-JUN-1999; 99GB-00012736.
XX
PA (DEVG-) DEVGEN NV.
PI Zwaal R, Groenen J, Bogaert T;
WPI; 2000-658082/64.
PT Identifying modulators of sarco/endoplasmic reticulum calcium ATPase,
PT useful potentially for treating disorders of calcium homeostasis, e.g.
PT cardiac hypertrophy.
PS
XX Disclosure; Fig 11; 108pp; English.
XX
XX The present invention is concerned with methods of using C. elegans to
XX identify compounds which are capable of up- and down-regulating the
XX activity of the sarco/endoplasmic reticulum calcium ATPase (SERCA). This
XX protein is involved in cell signalling, and elevated levels affect
XX cellular processes such as contraction, secretion and cell cycling. The

CC methods can be used to identify compounds for use in the treatment of
CC some muscle pathologies, cardiac hypertrophy, heart failure,
CC hypertension, diabetes, Darter-White disease and Brody's disease
XX

Sequence 159 BP, 45 A; 41 C; 22 G; 51 T; 0 U; 0 Other;

Query Match 37.6%; Score 50.8; DB 3; Length 159;
Best Local Similarity 68.6%; Pred. No. 6.9e-06;
Matches 70; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

17 AGAGCATGATGATTAATGCAATTCAGCAGAGGCGAGATGAGAAATGACAAAGCAATG 76
155 AGAAGCATGACAGATGATGCAATTCAGCAAGAGGCGATTAAGATGAGACAGAAATTGATA 96

77 AAAGCATTCGTGAGGCTTCGCTGCGCTGAGGCGCTTCTCTCA 118
95 AATAGCTTCTGAAAGGTTTGACGCTGCTTGTGAGGCAATTCA 54

RESULT 2

ADBS3082/C
ADBS3082 standard; DNA; 701 BP.

ADBS3082;

04-DEC-2003 (first entry)

Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3624.

toxic effect; gene expression profile; hepatotoxicity; diagnostic marker;
toxicity marker; toxicity progression; drug screening;
primary rat hepatocyte toxicity modelling; gene; de.

Rattus norvegicus.

MO2003065993-A2.

14-AUG-2003.

04-FEB-2003; 2003MO-US003482.

04-FEB-2002; 2002US-0353171P.
13-MAR-2002; 2002US-0363534P.
08-APR-2002; 2002US-0370248P.
10-APR-2002; 2002US-0371134P.
10-APR-2002; 2002US-0371135P.
10-APR-2002; 2002US-0371150P.
11-APR-2002; 2002US-0371413P.
19-APR-2002; 2002US-0373601P.
12-APR-2002; 2002US-0374139P.
08-MAY-2002; 2002US-0378370P.
09-MAY-2002; 2002US-0378652P.
09-MAY-2002; 2002US-0378653P.
09-MAY-2002; 2002US-0378665P.
09-JUL-2002; 2002US-0394230P.
09-JUL-2002; 2002US-0394253P.
04-SEP-2002; 2002US-0407688P.
28-JAN-2003; 2003US-0442900P.

(GENE-) GENE LOGIC INC.

Mendrick D, Porter M, Johnson K, Higgs B, Castle A, Orr M;
Elashoff M;

WPI; 2003-731472/69.

Determining if a compound induces a toxic effect on a tissue or cell, for
identifying hepatotoxic compounds, comprises comparing a gene expression
profile of a tissue or cell sample to a database of Tox mean and non-Tox
mean values.

Claim 44; SEQ ID NO 3624; 874bp; English.

XX The present invention describes a method for determining whether a
CC compound induces a toxic effect on a tissue or cell. The method comprises
CC preparing a gene expression profile of a tissue or cell sample exposed to
CC the compound, and comparing the gene expression profile to a database
CC comprising data or information on the Tox mean and non-Tox mean value.
CC The method is useful for predicting or identifying at least one toxic
CC effect, particularly hepatotoxicity, of a test or unknown compound. The
CC genes listed in the specification are useful as diagnostic or toxicity
CC markers for the prediction or identification of the physiological state
CC of tissue or cell sample that has been exposed to a compound, or to
CC identify or predict the toxic effects of a compound or an agent. These
CC may also be used as markers for monitoring toxicity progression or for
CC drug screening. The present sequence represents a primary rat hepatocyte
CC toxicity modelling related gene sequence from the present invention.

Sequence 701 BP, 184 A; 178 C; 141 G; 198 T; 0 U; 0 Other;
Query Match 37.2%; Score 50.2; DB 10; Length 701;
Best Local Similarity 68.0%; Pred. No. 1.7e-05;
Matches 70; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

16 CAGAGCATGACGATTAATGCAATTCAGCAGAGGCGAGATGAGAAATGACAAAGCAAT 75
329 CAGAGCATGACGATTAATGCAATTCAGCAGAGGCGAGATGAGAAATGAT 270

76 GAAAGCATTCGTGAGGCTTCGCTGCGCTGAGGCGCTTCTCTCA 118
269 AAGAGGTTCTGAGGTTTCTGACGCGCTTGTGCGGCAATTCA 227

RESULT 3

ADR97285/C
ADR97285 standard; DNA; 159 BP.

ADR97285;

16-DEC-2004 (first entry)

Human phospholamban polymorphism fragment DNA.

ds; human; phospholamban; polymorphism; cardiovascular disease.

Homo sapiens.

US2004191802-A1.

30-SEP-2004.

22-OCT-2003; 2003US-00691412.

22-OCT-2002; 2002US-0420295P.

(KRAN/) KRANTAS E. G.
(HAGH/) HAGHIGHT K.

Kranias EG, Haghighi K;

WPI; 2004-699841/67.

Phospholamban polymorphism assessment in individual, for determining risk
for developing cardiovascular disease, by comparing analysis of the
nucleotide fragment with a predetermined phospholamban nucleotide
fragment sequence.

Claim 15; SEQ ID NO 1; 15bp; English.

The invention relates to a method of phospholamban polymorphism
assessment in an individual which comprises comparing the analysis of the
nucleotide fragment with a predetermined phospholamban nucleotide
fragment sequence to determine whether the individual carries a
phospholamban polymorphism. The methods and phospholamban polymorphism
fragment are useful for determining if an individual is at risk for

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 7, 2005, 09:02:25 ; Search time 1691.67 Seconds
(without alignments)
3037.641 Million cell updates/sec

Title: US-10-724-532-6

Perfect score: 135
Sequence: 1 ctctctctctcgcagcagga.....tcacgatacagcttctctc 135

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hnc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gsa1:*
9: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Length	DB ID	Description
1	50.8	37.6	381	5	BX669692 BX669692
2	50.8	37.6	702	5	BX922974 BX922974
3	50.8	37.6	724	5	BX674983 BX674983
4	50.8	37.6	740	5	BX924154 BX924154
5	50.8	37.6	758	5	BX923697 BX923697
6	50.8	37.6	811	7	CK449263 CK449263
7	50.2	37.2	179	2	BE113353 BE113353
8	50.2	37.2	377	2	BF547322 BF547322
9	50.2	37.2	417	1	AI322542 AI322542
10	50.2	37.2	439	2	BE115006 BE115006
11	50.2	37.2	449	2	BF394968 BF394968
12	50.2	37.2	449	2	BE098177 BE098177
13	50.2	37.2	451	4	BI288911 BI288911
14	50.2	37.2	454	2	BE099930 BE099930
15	50.2	37.2	476	2	BF525258 BF525258
16	50.2	37.2	480	7	CR471116 CR471116
17	50.2	37.2	487	4	BC379827 BC379827
18	50.2	37.2	498	1	AI603160 AI603160
19	50.2	37.2	511	4	BF395370 BF395370
20	50.2	37.2	513	4	BI296789 BI296789
21	50.2	37.2	518	2	BE112568 BE112568
22	50.2	37.2	527	2	BF395607 BF395607
23	50.2	37.2	528	2	BF395670 BF395670
24	50.2	37.2	540	2	BF395398 BF395398

25	50.2	37.2	575	4	BI290034 BI290034
26	50.2	37.2	589	2	BF525010 BF525010
27	50.2	37.2	608	1	AI103929 AI103929
28	50.2	37.2	699	7	CK358482 CK358482
29	50.2	37.2	710	7	CK359590 CK359590
30	50.2	37.2	718	7	CK358464 CK358464
31	50.2	37.2	719	7	CK356296 CK356296
32	50.2	37.2	731	7	CK357243 CK357243
33	50.2	37.2	737	7	CK357232 CK357232
34	50.2	37.2	738	7	CK355359 CK355359
35	50.2	37.2	738	7	CK357123 CK357123
36	50.2	37.2	744	7	CK356439 CK356439
37	50.2	37.2	744	7	CK357747 CK357747
38	50.2	37.2	745	7	CK355314 CK355314
39	50.2	37.2	745	7	CK356371 CK356371
40	50.2	37.2	748	7	CK359219 CK359219
41	50.2	37.2	754	7	CK355445 CK355445
42	50.2	37.2	758	7	CK355453 CK355453
43	50.2	37.2	758	7	CK357746 CK357746
44	50.2	37.2	762	7	CK359188 CK359188
45	50.2	37.2	764	7	CK357447 CK357447

ALIGNMENTS

RESULT 1
BX669692/c 381 bp mRNA linear EST 07-MAY-2004
LOCUS BX669692 Sus Scrofa library (scac) Sus scrofa cDNA clone
DEFINITION scac00281.c.02 5prim, mRNA sequence.
ACCESSION BX669692
VERSION BX669692
KEYWORDS EST.
SOURCE BX669692.1 GI:37979481
ORGANISM Sus scrofa (pig)
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.

REFERENCE
Auteurs
Bonnet, A., Tosser-Klopp, G., Benne, F., Gabau, C., Villegier, S.,
Soares, M., Bonaldi, F. and Hately, F.
A Pig Normalised Multi-Tissue cDNA Library
Unpublished (2003)
Contact: Tosser-Klopp G
Genetique Animale
Institut National de la Recherche Agronomique
Chemin de Borde-Rouge - Auzeville BP27, 31326 Castanet-Tolosan
cedex, FRANCE
Tel: 33 (0) 5.61.28.51.14
Fax: 33 (0) 5.61.28.53.08
Email: tosser@toulouse.inra.fr
Sequence cleaned of vector, adaptor and repetitions. Contact us
at signa@inra.fr to obtain the chromatogram of this
sequence.

FEATURES
source
Plate: 0028 row: c column: 2.
Location/Qualifiers
1..381
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="scac00281.c.02"
/tissue_type="mixed"
/clone_lib="Sus Scrofa library (scac)"
/note="Vector: pRT3D-pac vector; tissues: adipose tissue,
brain, kidney, liver, muscle, ovary, testis, heart,
hypothalamus, pancreas, skin, spleen, thymus, placenta,
pituitary gland, seminal vesicle, small intestine,
uterus, adrenals, bulbo urethral gland, cerebral trunk,
epididymis, female gonad, gall-bladder, hippocampus,
large intestine, male gonad, melanocytes, stomach, udder"

Query Match

37.6% Score 50.8; DB 5; Length 381;

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Comugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 7, 2005, 09:02:25 ; Search time 77.2222 Seconds
(without alignments)
2860.541 Million cell updates/sec

Title: US-10-724-532-6
Perfect score: 135
Sequence: 1 cctctctcctcgcagcagga.....tcacgatacctctctc 135

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 81813359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/prodata/1/ina/5A.COMB.seq:*
- 2: /cgn2_6/prodata/1/ina/5B.COMB.seq:*
- 3: /cgn2_6/prodata/1/ina/6A.COMB.seq:*
- 4: /cgn2_6/prodata/1/ina/6B.COMB.seq:*
- 5: /cgn2_6/prodata/1/ina/PCITUS.COMB.seq:*
- 6: /cgn2_6/prodata/1/ina/Backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	50.8	37.6	159	4 US-09-549-872B-9	Sequence 9, Appl
C 2	50.8	37.6	159	4 US-09-549-872B-13	Sequence 13, Appl
C 3	46	34.1	1480	4 US-09-513-999C-10799	Sequence 10799, A
C 4	46	34.1	1635	4 US-09-949-016-1439	Sequence 1439, Ap
C 5	46	34.1	16062	4 US-09-949-016-13181	Sequence 13181, A
C 6	44.2	32.7	315	3 US-09-124-671-26	Sequence 26, Appl
C 7	35	25.9	6481	4 US-09-620-312D-1076	Sequence 1076, Ap
C 8	31.4	23.3	2175	4 US-08-914-999-3	Sequence 3, Appl
C 9	30.6	22.7	1917	4 US-09-902-540-3588	Sequence 3588, Ap
C 10	30.6	22.7	19394	4 US-09-902-540-1172	Sequence 1172, Ap
C 11	30.2	22.4	65424	4 US-09-949-016-12426	Sequence 12426, A
C 12	30.2	22.4	74353	4 US-09-949-016-15336	Sequence 15336, A
C 13	29.6	21.9	957	1 US-08-309-182B-1	Sequence 1, Appl
C 14	29.6	21.9	8590	4 US-09-949-016-5562	Sequence 5562, Ap
C 15	29.6	21.9	10300	4 US-09-949-016-636	Sequence 636, App
C 16	29.6	21.9	38575	4 US-09-949-016-12378	Sequence 12378, A
C 17	29.6	21.9	11935	4 US-09-949-016-12704	Sequence 12704, A
C 18	29.2	21.6	1095	4 US-09-252-991A-14880	Sequence 14880, A
C 19	29.2	21.6	1317	4 US-09-552-991A-17748	Sequence 14748, A
C 20	29.2	21.6	2622	4 US-09-552-991A-15001	Sequence 15001, A
C 21	29	21.5	474	4 US-09-513-999C-1161	Sequence 1161, Ap
C 22	29	21.5	601	4 US-09-549-016-202802	Sequence 202802,
C 23	29	21.5	1123	3 US-09-188-930-28	Sequence 28, Appl
C 24	29	21.5	1123	3 US-09-188-930-203	Sequence 203, Appl
C 25	29	21.5	1123	4 US-09-512-283C-28	Sequence 28, Appl
C 26	29	21.5	1123	4 US-09-512-283C-203	Sequence 203, App
C 27	29	21.5	26050	4 US-09-949-016-17449	Sequence 17449, A

C 28	28.8	21.3	879	4 US-09-489-039A-5041	Sequence 5041, Ap
C 29	28.6	21.2	601	4 US-09-949-016-200644	Sequence 200644,
C 30	28.6	21.2	601	4 US-09-949-016-200790	Sequence 200790,
C 31	28.6	21.2	46343	4 US-09-949-016-16824	Sequence 16824, A
C 32	28.6	21.2	152582	4 US-09-949-016-12086	Sequence 12086, A
C 33	28.6	21.2	152583	4 US-09-949-016-17390	Sequence 17390, A
C 34	28.6	21.2	152583	4 US-09-949-016-17391	Sequence 17391, A
C 35	28.6	21.2	1664976	4 US-08-916-421B-1	Sequence 1, Appl
C 36	28.6	21.2	1664976	4 US-09-692-570-1	Sequence 1, Appl
C 37	28.4	21.0	1855	4 US-09-949-016-1929	Sequence 1929, Ap
C 38	28.4	21.0	162914	4 US-09-949-016-15578	Sequence 15578, A
C 39	28.2	20.9	568	4 US-08-956-171E-999	Sequence 999, App
C 40	28.2	20.9	568	4 US-08-781-986A-999	Sequence 999, App
C 41	28.2	20.9	603	3 US-08-816-346-5	Sequence 5, Appl
C 42	28.2	20.9	603	3 US-09-335-411-5	Sequence 1, Appl
C 43	28.2	20.9	1851	4 US-09-949-016-3036	Sequence 3036, Ap
C 44	28.2	20.9	2120	4 US-09-149-476-160	Sequence 160, App
C 45	28.2	20.9	2907	3 US-08-816-346-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-09-549-872B-9/C
Sequence 9, Application US/09549872B
Patent No. 6540996
GENERAL INFORMATION:
APPLICANT: Zwaal, Richard
APPLICANT: Groenen, Jose
TITLE OF INVENTION: COMPOUND SCREENING METHODS
FILE REFERENCE: D00590/70008 (JRV/RE)
CURRENT APPLICATION NUMBER: US/09/549, 872B
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: GB 9908670.4
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: US 60/129, 596
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: GB 9912736.7
PRIOR FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 9
LENGTH: 159
TYPE: DNA
ORGANISM: Sus sp.
US-09-549-872B-9

Query Match
Best Local Similarity 37.6%; Score 50.8; DB 4; Length 159;
Matches 70; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 17 AGAGCATGACCATATGCAATTCAGCAGGAGCAGATGATGATGACAAAGCAATG 76
|||
DB 155 AAGACATACATGATGCAATTCAGCAAGGCAATTAATGATGACAGAAATGATA 96
|||

QY 77 AAAGCATTCGAGGTTCTGCTGCGCTGAGGCTTCTTCA 118
|||
DB 95 AATGAGTTCTGAAGGTTTGAAGTCTGTTGAGCATTTCA 54
|||

RESULT 2
US-09-549-872B-13/C
Sequence 13, Application US/09549872B
Patent No. 6540996
GENERAL INFORMATION:
APPLICANT: Zwaal, Richard
APPLICANT: Groenen, Jose
TITLE OF INVENTION: COMPOUND SCREENING METHODS
FILE REFERENCE: D00590/70008 (JRV/RE)
CURRENT APPLICATION NUMBER: US/09/549, 872B

```
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: GB 9908670.4
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: US 60/129,596
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: GB 9912736.7
; PRIOR FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 159
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HUMANIZED PIG
; OTHER INFORMATION: PIG CDNA
US-09-549-872B-13
```

```
Query Match          37.6%; Score 50.8; DB 4; Length 159;
Best Local Similarity 68.6%; Pred. No. 1.2e-07;
Matches 70; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
```

```
QY 17 AGAGCATGACGATPAATGCAATCAGCAGAGGCGATGAGATCAGCAAAAAGCAATG 76
    |||||
DB 155 AGAAGCATCAGATGATCAATCAGCAAGGCGATATTAGATGAGCAGAAATTGATA 96
    |||||
QY 77 AAAGATTCTGAGGTTCTGCTGGCCCTGAGGCTTCTCTCA 118
    |||||
DB 95 AATAGTTCTGAAAGTTTGAAGTCTGTTGAGGCATTTC 54
    |||||
```

RESULT 3

```
US-09-513-999C-10799/C
; Sequence 10799, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclet, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59, US2, REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 10799
; LENGTH: 480
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-10799
```

```
Query Match          34.1%; Score 46; DB 4; Length 480;
Best Local Similarity 65.7%; Pred. No. 8.4e-06;
Matches 67; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
```

```
QY 17 AGAGCATGACGATPAATGCAATCAGCAGAGGCGATGAGATCAGCAAAAAGCAATG 76
    |||||
DB 350 AGAAGCATCAGATGATCAATCAGCAAGAGCATATTAGATGAGCAGAAATTGATA 291
    |||||
QY 77 AAAGATTCTGAGGTTCTGCTGGCCCTGAGGCTTCTCTCA 118
    |||||
DB 290 AATGATTCTGAGCTTTTGAAGTCTGTTGAGGCATTTC 249
    |||||
```

RESULT 4

```
US-09-949-016-1439/C
; Sequence 1439, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
```

```
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1439
; LENGTH: 1635
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1439
```

```
Query Match          34.1%; Score 46; DB 4; Length 1635;
Best Local Similarity 65.7%; Pred. No. 1.5e-05;
Matches 67; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
```

```
QY 17 AGAGCATGACGATPAATGCAATCAGCAGAGGCGATGAGATCAGCAAAAAGCAATG 76
    |||||
DB 336 AGAAGCATCAGATGATCAATCAGCAAGGCGATATTAGATGAGCAGAAATTGATA 277
    |||||
QY 77 AAAGATTCTGAGGTTCTGCTGGCCCTGAGGCTTCTCTCA 118
    |||||
DB 276 AATGATTCTGAGCTTTTGAAGTCTGTTGAGGCATTTC 235
    |||||
```

RESULT 5

```
US-09-949-016-13181/C
; Sequence 13181, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13181
; LENGTH: 16062
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13181
```

```
Query Match          34.1%; Score 46; DB 4; Length 16062;
Best Local Similarity 65.7%; Pred. No. 4.2e-05;
Matches 67; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
```

```
QY 17 AGAGCATGACGATPAATGCAATCAGCAGAGGCGATGAGATCAGCAAAAAGCAATG 76
    |||||
DB 12762 AGAAGCATCAGATGATCAATCAGCAAGAGCATATTAGATGAGCAGAAATTGATA 12703
    |||||
QY 77 AAAGATTCTGAGGTTCTGCTGGCCCTGAGGCTTCTCTCA 118
    |||||
DB 12702 AATGATTCTGAGCTTTTGAAGTCTGTTGAGGCATTTC 12661
    |||||
```

RESULT 6

```
US-09-124-671-26/C
; Sequence 26, Application US/09124671A
```


	80.0%: Score 108; DB 20;	Length 108;
Query Match Similarity	100.0%;	Pred. No. 1.1e-26;
Best Local Similarity	0;	Mismatches 0; Indels 0;
Matches 108; Conservative		Gaps 0;

16 CAGAGCATGACGATTAATTCGAATCAGCGAGGCGCATGAGAAATCAGCAAAAAGCAT 75

Query Match	37.6%	Score 50.8	DB 15	Length 159
Best Local Similarity	68.6%	Pred. No. 4.2e-07		
Matches 70; Conservative	0	Mismatches 32	Indels 0	Gaps 0